SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Griffeth, Irwin J.; Pollock, Joanne; Bond, Julian F.; Garman, Richard D; Kuo, Mei-Chang; Yeung, Siu-mei H.; Brauer, Andrew; Exley, Mark A.;
- (ii) TITLE OF INVENTION: Allergenic Proteins And Peptides From Japanese Cedar Pollen

Powers, Steven P.

- (iii) NUMBER OF SEQUENCES: 201
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: ImmuLogic Pharmaceutical Corporation, Inc. (B) STREET: 610 Lincoln St

 - (C) CITY: Waltham
 - (D) STATE: MA
 - COUNTRY: USA
 - (F) ZIP: 02154
 - (v) COMPUTER READABLE FORM:

 - (A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US93/00139 (B) FILING DATE: January 15, 1993 (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/938,990(B) FILING DATE: September 1, 1992
- (viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: Darlene A. Vanstone

 - (B) REGISTRATION NUMBER: 35,729 (C) REFERENCE/DOCKET NUMBER: 025.5 US (IMI-028PC)
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1337 base pairs (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Crytpomeria japonica
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 66..1187
 - (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide (B) LOCATION: 129 1187





SEQUENCE LISTING

5	(1) GENE	RAL INFORMATION:
3	(i)	APPLICANT: Griffith, Irwin J. et al.
10	(ii)	TITLE OF INVENTION: Allergenic Proteins And Peptides From Japanese Cedar Pollen
	(iii)	NUMBER OF SEQUENCES: 195
15	(iv)	CORRESPONDENCE ADDRESS: (A) ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION (B) STREET: 610 Lincoln Street (C) CITY: Waltham (D) STATE: MA (E) COUNTRY: USA
		(F) ZIP: 02154
25	(V)	COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/M9-DOS (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
30	(vi)	CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: (B) FILING DATE: (C) CLASSIFICATION:
35	(vii)	PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: 07/938,990 (B) FILING DATE: September 1, 1992
40	(viii)	ATTORNEY/AGENT INFORMATION: (A) NAME: Darlene A. Vanstone (B) REGISTRATION NUMBER: 35,729 (C) REFERENCE/DOCKET NUMBER: 025.5 US
45	(ix)	TELECOMMUNICATION INFORMATION: (A) TELEPHONE: (617) 466-6000 (B) TELEFAX: (617) 466-6040
	(2) INFO	RMATION FOR SEQ ID NO:1:
50	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 1337 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
55	(ii)	MOLECULE TYPE: cDNA to mRNA
60	(vi)	ORIGINAL SOURCE: (A) ORGANISM: Crytpomeria japonica
60	(j/x)	FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 661187
65	(ix)	FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION: 1291187





(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	AGTO	CAATO	CTG (CTCAT	TAATO	CA TA	AGCA	ragco	GT#	ATAGA	AAAG	AAAT	TTCT	ACA C	CTCTC	CTACC		60
5	AAA			sp Se					al Al	CA TT la Le			al Ph					107
10		ATT Ile																155
15		GAC Asp																203
20		GGC Gly																251
20		GTC Val																299
25		CGC Arg																347
30		AAT Asn 75																395
35		ACT Thr															•	443
40		TGT Cys																491
40		CTG Leu																539
45		AGT Ser																587
50		CTG Leu 155																635
55		TCT Ser																683
60		ATT Ile																731
60		CAT His																779
65		TTC Phe																827
70		TAT Tyr 235																875





5						GGG Gly 255											92	23
3	AAT Asn	AGT Ser	TTC Phe	ACT Thr	GCA Ala 270	CCA Pro	AAT Asn	GAG Glu	AGC Ser	TAC Tyr 275	AAG Lys	AAG Lys	CAA Gln	GTA Val	ACC Thr 280	ATA Ile	9'	71
10						ACA Thr											10	19
15						TTT Phe											10	67
20						AAT Asn											11:	15
25						ACT Thr 335											110	63
20						AAA Lys			TGA	rgato	GCA :	rata:	PTCT	AG CZ	ATGT:	FGTAC	12	17
30	TAT	CTAA	ATT A	AACA	ГСАА	CA AC	GAAA	ATATA	A TC	ATGA	IGTA	TAT	rgttv	GTA :	rtga:	IGTCAA	12	77
	AATA	AAAA	ATG :	ratc:	TTTT?	AC T	ATTA	AAAA	A AA	YTAAA	GATC	GAT	CGGA	CGG :	racc'	TCTAGA	133	37
35	(2)	INF	ORMA	rion	FOR	SEQ	ID 1	10:2	:									
			(i) s			CHAI NGTH					~							
40				(B)	TYI	PE: 8	amino	ac	iđ	acrus	5							
40		(·	ii) N			ТҮРІ												
						DESC	_			מד כ	NO:2	2 •						
45	Met					Leu							Ser	Phe	Val	Ile		
		-20				_	-15					-10						
50	Gly -5	Ser	Cys	Phe	Ser	Asp 1	Asn	Pro	Ile	Asp 5	Ser	Cys	Trp	Arg	Gly 10	Asp		
	Ser	Asn	Trp	Ala 15	Gln	Asn	Arg	Met	Lys 20	Leu	Ala	Asp	Cys	Ala 25	Val	Gly		
55	Phe	Gly	Ser 30	Ser	Thr	Met	Gly	Gly 35	Lys	Gly	Gly	Asp	Leu 40	Tyr	Thr	Val		
60	Thr	Asn 45	Ser	Asp	Asp	Asp	Pro 50	Val	Asn	Pro	Ala	Pro 55	Gly	Thr	Leu	Arg		
00	Tyr 60	Gly	Ala	Thr	Arg	Asp 65	Arg	Pro	Leu	Trp	Ile 70	Ile	Phe	Ser	Gly	Asn 75		
65	Met	Asn	Ile	Lys	Leu 80	Lys	Met	Pro	Met	Tyr 85	Ile	Ala	Gly	Tyr	Lys 90	Thr		
	Phe	Asp	Gly	Arg 95	Gly	Ala	Gln	Val	Tyr 100	Ile	Gly	Asn	Gly	Gly 105	Pro	Cys		
70	Val	Phe	Ile 110	Lys	Arg	Val	Ser	Asn 115	Val	Ile	Ile	His	Gly 120	Leu	Tyr	Leu		





	Тyr	125	Cys	Ser	Thr	Ser	Val 130	Leu	Gly	Asn	Val	Leu 135	Ile	Asn	Glu	Ser	
5	Phe 140	Gly	Val	Glu	Pro	Val 145	His	Pro	Gln	Asp	Gly 150	Asp	Ala	Leu	Thr	Leu 155	
	Arg	Thr	Ala	Thr	Asn 160	Ile	Trp	Ile	Asp	His 165	Asn	Ser	Phe	Ser	Asn 170	Ser	
10	Ser	Asp	Gly	Leu 175	Val	Asp	Val	Thr	Leu 180	Thr	Ser	Thr	Gly	Val 185		Ile	
15	Ser	Asn	Asn 190	Leu	Phe	Phe	Asn	His 195	His	Lys	Val	Met	Leu 200	Leu	Gly	His	
	Asp	Asp 205	Ala	Tyr	Ser	Asp	Asp 210	Lys	Ser	Met	Lys	Val 215	Thr	Val	Ala	Phe	
20	Asn 220	Gln	Phe	Gly	Pro	Asn 225	Cys	Gly	Gln	Arg	Met 230	Pro	Arg	Ala	Arg	Tyr 235	
25	Gly	Leu	Val	His	Val 240	Ala	Asn	Asn	Asn	Tyr 245	Asp	Pro	Trp	Thr	Ile 250	Tyr	
23	Ala	Ile	Gly	Gly 255	Ser	Ser	Asn	Pro	Thr 260	Ile	Leu	Ser	Glu	Gly 265	Asn	Ser	
30	Phe	Thr	Ala 270	Pro	Asn	Glu	Ser	Туг 275	Lys	Lys	Gln	Val	Thr 280	Ile	Arg	Ile	
	Gly	Cys 285	Lys	Thr	Ser	Ser	Ser 290	Cys	Ser	Asn	Trp	Val 295	Trp	Gln	Ser	Thr	
35	Gln 300	Asp	Val	Phe	Tyr	Asn 305	Gly	Ala	Tyr	Phe	Val 310	Ser	Ser	Gly	Lys	Tyr 315	
40	Glu	Gly	Gly	Asn	Ile 320	Tyr	Thr	Lys	Lys	Glu 325	Ala	Phe	Asn	Val	Glu 330	Asn	
•0	Gly	Asn	Ala	Thr 335	Pro	Gln	Leu	Thr	Lys 340	Asn	Ala	Gly	Val	Leu 345	Thr	Cys	
45	Ser	Leu	Ser 350	Lys	Arg	Cys											
	(2)	INF	'AMAC	rion	FOR	SEQ	ID I	10:3	:								
50		(i)	() () ()		ENGTI PE: PRANI	H: 17 nuc DEDNI	7 bas leic ESS:	se pa acio sino	airs 1								
55		(xi)) SE	QUENC	CE DE	ESCR	[PTIC	N: S	SEQ I	ID NO	0:3:						
	GAY	AAYC	CNA '	THGA:	WS												17
60	(2)			rion													
65		(1	() () ()	QUENC A) LI B) T' C) S' O) T(ENGTI (PE: PRANI	H: 25 nucl	bas leic ESS:	se pa acio sing	airs 1								
<i>03</i>		(xi	,	QUENC					SEO -	ED NO	0:4:						
70	GGG			YTGG					- z ·		- 						25



	(2)	INFO	RMATION FOR SEQ ID NO:5:	
5		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
10		(ix)	FEATURE: (A) NAME/KEY: modified_base (B) LOCATION: 15 (D) OTHER INFORMATION: /mod_base= i	
15		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:5:	
13	CTG	CAGCC	RT TYTCNACRTT RAA	23
	(2)	INFO	RMATION FOR SEQ ID NO:6:	
20 25		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
30		(ix)	FEATURE: (A) NAME/KEY: modified_base (B) LOCATION: 6 (D) OTHER INFORMATION: /mod_base= i	·
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:6:	
	TTC		RT TYTGNGCCCA	20
35	(2)	INFO	RMATION FOR SEQ ID NO:7:	
40		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
4.~		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:7:	
45	CCTC	GCAGC1	KR TTYTGNGCCC AARTT	25
	(2)	INFO	RMATION FOR SEQ ID NO:8:	
50		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
55		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:8:	
	ATGO		CC CTTGCTTA	18
60	(2)	INFO	RMATION FOR SEQ ID NO:9:	
65			SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:9:	
70	GGG	ATTC	GA TAATCCCATA GACAGC	26
	(2)	TNFO	RMATION FOR SEC ID NO.10.	



5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	4
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:	
10	ATGCCTATGT ACATTGC	17
10	(2) INFORMATION FOR SEQ ID NO:11:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:	
20	GCAATGTACA TAGGCAT	17
	(2) INFORMATION FOR SEQ ID NO:12:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
	TCCAATTCTT CTGATGGT	18
35	(2) INFORMATION FOR SEQ ID NO:13:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
45	TTTTGTCAAT TGAGGAGT	18
	(2) INFORMATION FOR SEQ ID NO:14:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	
	CCTGCAGAAG CTTCATCAAC AACGTTTAGA	30
60	(2) INFORMATION FOR SEQ ID NO:15:	
65	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
70	TAGCAACTCC AGTCGAAGT	19
	(2) INFORMATION FOR SEO ID NO:16:	



5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	
10	TAGCTCTCAT TTGGTGC	17
	(2) INFORMATION FOR SEQ ID NO:17:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
20	TATGCAATTG GTGGGAGT	18
	(2) INFORMATION FOR SEQ ID NO:18:	
25	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: peptide	
	(v) FRAGMENT TYPE: N-terminal	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: Cryptomeria japonica	
40	<pre>(ix) FEATURE: (A) NAME/KEY: Modified-site (B) LOCATION: 7 (D) OTHER INFORMATION: /note= "the amino acid at position 7 is Ser, Cys, Thr, or His"</pre>	·
4.5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
45	Asp Asn Pro Ile Asp Ser Xaa Trp Arg Gly Asp Ser Asn Trp Ala Gln 1 5 10 15	
50	Asn Arg Met Lys	
	(2) INFORMATION FOR SEQ ID NO:19:	
55	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 16 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
60	(ii) MOLECULE TYPE: peptide	
60	(v) FRAGMENT TYPE: internal	
65	<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Cryptomeria japonica</pre>	
05	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:	
70	Glu Ala Phe Asn Val Glu Asn Gly Asn Ala Thr Pro Gln Leu Thr Lys 1 10 15	
, 0	(2) INFORMATION FOR SEQ ID NO:20:	

(i) SEQUENCE CHARACTERISTICS:



5	(A) LENGTH: 30 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
3	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:	
	GGGTCTAGAG GTACCGTCCG ATCGATCATT	30
10	(2) INFORMATION FOR SEQ ID NO:21:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	•
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:	
20	GGGTCTAGAG GTACCGTCCG	20
	(2) INFORMATION FOR SEQ ID NO:22:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:	
	AATGATCGAT GCT	13
35	(2) INFORMATION FOR SEQ ID NO:23:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
45	GGAATTCTCT AGACTGCAGG T	21
45	(2) INFORMATION FOR SEQ ID NO:24:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:	
33	GGAATTCTCT AGACTGCAGG TTTTTTTTTT TTTTTT	35
	(2) INFORMATION FOR SEQ ID NO:25:	
60	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 5 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
65	(ii) MOLECULE TYPE: peptide	
	(v) FRAGMENT TYPE: N-terminal	
70	<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Juniperus sabinoides</pre>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	



Asp Asn Pro Ile Asp

- 5 (2) INFORMATION FOR SEQ ID NO:26:
 - (i) SEQUENCE CHARACTERISTICS:
 - (Ã) LENGTH: 20 amino acids
 - (B) TYPE: amino acid (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (v) FRAGMENT TYPE: internal
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Asp Asn Pro Ile Asp Ser Cys Trp Arg Gly Asp Ser Asn Trp Ala Gln

Asn Arg Met Lys

10

15

20

25

65

- (2) INFORMATION FOR SEQ ID NO:27:
 - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid
- (D) TOPOLOGY: linear 30
 - (ii) MOLECULE TYPE: peptide
 - (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27: 35

Asp Ser Asn Trp Ala Gln Asn Arg Met Lys Leu Ala Asp Cys Ala Val

- 40 Gly Phe Gly Ser
 - (2) INFORMATION FOR SEQ ID NO:28:
- 45 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: peptide
 - (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28: 55

Leu Ala Asp Cys Ala Val Gly Phe Gly Ser Ser Thr Met Gly Gly Lys 10

- Gly Gly Asp Leu 60 20
 - (2) INFORMATION FOR SEQ ID NO:29:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
- 70 (v) FRAGMENT TYPE: internal





		(XI) SEQUENCE DESCRIPTION: SEQ ID NO:29:
5	Ser 1	Thr Met Gly Gly Lys Gly Gly Asp Leu Tyr Thr Val Thr Asn Ser
	Asp	Asp Asp Pro 20
10	(2)	INFORMATION FOR SEQ ID NO:30:
15		(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear
		(ii) MOLECULE TYPE: peptide
20		(v) FRAGMENT TYPE: internal
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
25	Tyr 1	Thr Val Thr Asn Ser Asp Asp Asp Pro Val Asn Pro Ala Pro Gly 5
25	Thr	Leu Arg Tyr 20
30	(2)	INFORMATION FOR SEQ ID NO:31:
30		(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid
35		(D) TOPOLOGY: linear
		(ii) MOLECULE TYPE: peptide
40		(v) FRAGMENT TYPE: internal
40	1	(X1) SEQUENCE DESCRIPTION: SEQ ID NO:31:
	val 1	Asn Pro Ala Pro Gly Thr Leu Arg Tyr Gly Ala Thr Arg Asp Arg 5 10 15
45	Pro	Leu Trp Ile
	(2)	20 INFORMATION FOR SEQ ID NO:32:
50		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear
55		(ii) MOLECULE TYPE: peptide
		(v) FRAGMENT TYPE: internal
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
60	Gly 1	Ala Thr Arg Asp Arg Pro Leu Trp Ile Ile Phe Ser Gly Asn Met 5 10 15
65	Asn	Ile Lys Leu 20
	(2)	INFORMATION FOR SEQ ID NO:33:
70		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear





	((ii) MOLECULE TYPE: peptide
_		(v) FRAGMENT TYPE: internal
5	((xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
10	Ile F 1	Phe Ser Gly Asn Met Asn Ile Lys Leu Lys Met Pro Met Tyr Ile 5 10 15
10	Ala G	Cly Tyr Lys 20
15	(2) I	INFORMATION FOR SEQ ID NO:34:
		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear
20	((ii) MOLECULE TYPE: peptide
		(v) FRAGMENT TYPE: internal
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
	Lys M 1	Met Pro Met Tyr Ile Ala Gly Tyr Lys Thr Phe Asp Gly Arg Gly 5 10 15
30	Ala G	Sin Val Tyr 20
	(2) I	NFORMATION FOR SEQ ID NO:35:
35		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear
40	(ii) MOLECULE TYPE: peptide
		(v) FRAGMENT TYPE: internal
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
	Thr F 1	Phe Asp Gly Arg Gly Ala Gln Val Tyr Ile Gly Asn Gly Gly Pro 5 10 15
50	Cys V	Val Phe Ile 20
	(2) I	NFORMATION FOR SEQ ID NO:36:
55		(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: peptide
60		(v) FRAGMENT TYPE: internal
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:
65	Ile G 1	Gly Asn Gly Gly Pro Cys Val Phe Ile Lys Arg Val Ser Asn Val 5 10 15
	Ile I	le His Gly 20
70	(2) I	INFORMATION FOR SEQ ID NO:37:
		(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids





(B) TYPE: amino acid (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: peptide	
(v) FRAGMENT TYPE: internal	
(xi) SEQUENCE DESCRIPTION: SEQ	ID NO:37:

Lys Arg Val Ser Asn Val Ile Ile His Gly Leu Tyr Leu Tyr Gly Cys 1 10 1510

> Ser Thr Ser Val 20

15

20

25

60

65

70

- (2) INFORMATION FOR SEQ ID NO:38:
 - (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 amino acids(B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:
- Leu Tyr Leu Tyr Gly Cys Ser Thr Ser Val Leu Gly Asn Val Leu Ile 30 10

Asn Glu Ser Phe 20

- 35 (2) INFORMATION FOR SEQ ID NO:39:
 - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear
- 40
 - (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal 45
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:
- Leu Gly Asn Val Leu Ile Asn Glu Ser Phe Gly Val Glu Pro Val His 50 Pro Gln Asp Gly
- 55 (2) INFORMATION FOR SEQ ID NO:40:
 - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (v) FRAGMENT TYPE: internal
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:
 - Gly Val Glu Pro Val His Pro Gln Asp Gly Asp Ala Leu Thr Leu Arg
 - Thr Ala Thr Asn





	(2)	INFORMATION FOR SEQ ID NO:41:
5		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear
		(ii) MOLECULE TYPE: peptide
10		(v) FRAGMENT TYPE: internal
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:
15	Asp 1	Ala Leu Thr Leu Arg Thr Ala Thr Asn Ile Trp Ile Asp His Asn 10 15
	Ser	Phe Ser Asn 20
20	(2)	INFORMATION FOR SEQ ID NO:42:
25		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear
		(ii) MOLECULE TYPE: peptide
30		(v) FRAGMENT TYPE: internal
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:
35	Ile 1	Trp Ile Asp His Asn Ser Phe Ser Asn Ser Ser Asp Gly Leu Val
	Asp	Val Thr Leu 20
40	(2)	INFORMATION FOR SEQ ID NO:43:
-1 0		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear
45		(ii) MOLECULE TYPE: peptide
		(v) FRAGMENT TYPE: internal
50		
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:
55	Ser 1	Ser Asp Gly Leu Val Asp Val Thr Leu Thr Ser Thr Gly Val Thr 5 10
	Ile	Ser Asn Asn 20
60	(2)	INFORMATION FOR SEQ ID NO:44:
65		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear
		(ii) MOLECULE TYPE: peptide
=0		(v) FRAGMENT TYPE: internal
70		(vi) CECULENCE DESCRIPTION, CEC ID NO.44.





	Thr 1	Ser Thr Gly Val Thr Ile Ser Asn Asn Leu Phe Phe Asn His His 5 10 15
5	Lys	Val Met Leu 20
	(2)	INFORMATION FOR SEQ ID NO:45:
10		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear
15		(ii) MOLECULE TYPE: peptide
		(v) FRAGMENT TYPE: internal
20		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:
20	Leu 1	Phe Phe Asn His His Lys Val Met Leu Leu Gly His Asp Asp Ala 5 10 15
25	Tyr	Ser Asp Asp 20
	(2)	INFORMATION FOR SEQ ID NO:46:
30		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear
35		(ii) MOLECULE TYPE: peptide
33		(v) FRAGMENT TYPE: internal
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:
40	Leu 1	Gly His Asp Asp Ala Tyr Ser Asp Asp Lys Ser Met Lys Val Thr 5 10 15
45	Val	Ala Phe Asn 20
	(2)	INFORMATION FOR SEQ ID NO:47:
50		(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids
		(B) TYPE: amino acid (D) TOPOLOGY: linear
55		(ii) MOLECULE TYPE: peptide
		(v) FRAGMENT TYPE: internal
60		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:
	Lys 1	Ser Met Lys Val Thr Val Ala Phe Asn Gln Phe Gly Pro Asn Cys 5 10 15
65	Gly	Gln Arg Met 20
	(2)	INFORMATION FOR SEQ ID NO:48:
70		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear





		(ii) MOLECULE TYPE: peptide
		(v) FRAGMENT TYPE: internal
5		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:
	Gln 1	Phe Gly Pro Asn Cys Gly Gln Arg Met Pro Arg Ala Arg Tyr Gly 5 10 15
10	Leu	Val His Val 20
	(2)	INFORMATION FOR SEQ ID NO:49:
15		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear
20		(ii) MOLECULE TYPE: peptide
		(v) FRAGMENT TYPE: internal
25		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:
23	Pro 1	Arg Ala Arg Tyr Gly Leu Val His Val Ala Asn Asn Asn Tyr Asp 5 10 15
30	Pro	Trp Thr Ile 20
	(2)	INFORMATION FOR SEQ ID NO:50:
35		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear
40		(ii) MOLECULE TYPE: peptide
-10		(v) FRAGMENT TYPE: internal
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:
45	Ala 1	Asn Asn Asn Tyr Asp Pro Trp Thr Ile Tyr Ala Ile Gly Gly Ser 5 10 15
	Ser	Asn Pro Thr 20
50	(2)	INFORMATION FOR SEQ ID NO:51:
55		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear
		(ii) MOLECULE TYPE: peptide
60		(v) FRAGMENT TYPE: internal
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:
65	Tyr 1	Ala Ile Gly Gly Ser Ser Asn Pro Thr Ile Leu Ser Glu Gly Asn 5 10 15
	Ser	Phe Thr Ala 20
70	(2)	INFORMATION FOR SEQ ID NO:52:
		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 amino acids





- (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 5 (v) FRAGMENT TYPE: internal (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:
- 10 Ile Leu Ser Glu Gly Asn Ser Phe Thr Ala Pro Asn Glu Ser Tyr Lys

Lys Gln Val Thr

15

20

40

45

55

60

65

- (2) INFORMATION FOR SEQ ID NO:53:
 - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids

 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
- 25 (v) FRAGMENT TYPE: internal
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:
- Pro Asn Glu Ser Tyr Lys Lys Gln Val Thr Ile Arg Ile Gly Cys Lys 30

Thr Ser Ser Ser

- 35 (2) INFORMATION FOR SEQ ID NO:54:
 - (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 amino acids(B) TYPE: amino acid

 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (v) FRAGMENT TYPE: internal
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Ile Arg Ile Gly Cys Lys Thr Ser Ser Ser Cys Ser Asn Trp Val Trp 10

50 Gln Ser Thr Gln

- (2) INFORMATION FOR SEQ ID NO:55:
 - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (v) FRAGMENT TYPE: internal
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Cys Ser Asn Trp Val Trp Gln Ser Thr Gln Asp Val Phe Tyr Asn Gly

70 Ala Tyr Phe Val





	(2)	INFORMATION FOR SEQ ID NO:56:
5		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear
		(ii) MOLECULE TYPE: peptide
10		(v) FRAGMENT TYPE: internal
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:
15	Asp 1	Val Phe Tyr Asn Gly Ala Tyr Phe Val Ser Ser Gly Lys Tyr Glu
	Gly	Gly Asn Ile 20
20	(2)	INFORMATION FOR SEQ ID NO:57:
25		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear
		(ii) MOLECULE TYPE: peptide
30		(v) FRAGMENT TYPE: internal
50		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:
35	Ser 1	Ser Gly Lys Tyr Glu Gly Gly Asn Ile Tyr Thr Lys Lys Glu Ala
	Phe	Asn Val Glu 20
40	(2)	INFORMATION FOR SEQ ID NO:58:
		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear
45		(ii) MOLECULE TYPE: peptide
		(v) FRAGMENT TYPE: internal
50		
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:
55	Tyr 1	Thr Lys Lys Glu Ala Phe Asn Val Glu Asn Gly Asn Ala Thr Pro
	Gln	Leu Thr Lys 20
60	(2)	INFORMATION FOR SEQ ID NO:59:
65		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear
		(ii) MOLECULE TYPE: peptide
		(v) FRAGMENT TYPE: internal
70		(xi) SEQUENCE DESCRIPTION: SEQ ID NO.59:





	Asn 1	Gly	Asn	Ala	Thr 5	Pro	Gln	Leu	Thr	Lys 10	Asn	Ala	Gly	Val	Leu 15	Thr
5	Cys	Ser	Leu	Ser 20												
	(2)	INFO	ORMA	rion	FOR	SEQ	ID 1	10:6	0:							
10		(i)	(1	A) LI B) T	ENGTI	HARAG H: 13 amin OGY:	3 ami	ino a cid		5						
15		(ii)	MOI	LECUI	LE T	YPE:	pept	tide								
••		(v)	FR2	AGMEI	T TV	YPE:	inte	erna:	1							
		(xi)) SE	QUEN	CE D	ESCR:	IPTIC	ON:	SEQ :	ID N	0:60	:				
20	Asn 1	Ala	Gly	Val	Leu 5	Thr	Cys	Ser	Leu	Ser 10	Lys	Arg	Cys			
	(2)	INF	ORMA	rion	FOR	SEQ	ID 1	.0 : 6	1:							
25		(i)	(<u>i</u>	A) L1 B) T	ENGTI	HARAG H: 60 amin OGY:	o ami	ino a		3	·					
30		(ii)	MOI	LECUI	LE T	YPE:	pept	tide								
		(v)	FRA	AGMEI	T TV	YPE:	inte	erna	1							
35		(xi)	SE	QUEN	CE DI	ESCR	IPTIC	ON:	SEQ :	ID N	0:61	:				
33	Asp 1	Asn	Pro	Ile	Asp 5	Ser	Cys	Trp	Arg	Gly 10	Asp	Ser	Asn	Trp	Ala 15	Gln
40	Asn	Arg	Met	Lys	Asp 20	Ser	Asn	Trp	Ala	Gln 25	Asn	Arg	Met	Lys	Leu 30	Ala
	Asp	Cys	Ala	Val 35	Gly	Phe	Gly	Ser	Ser 40	Thr	Met	Gly	Gly	Lys 45	Gly	Gly
45	Asp	Leu	Tyr 50	Thr	Val	Thr	Asn 55	Ser	Asp	Asp	Asp	Pro 60				
	(2)	INF	ORMA	TION	FOR	SEQ	ID 1	NO: 62	2:							
50		(i)	(1	A) LI B) T	ENGTI YPE:	HARA(H: 6(amin OGY:	o ami	ino a cid		5						
55		(ii)	MOI	LECUI	LE T	YPE:	pept	tiđe								
		(v)	FR2	AGMEI	T TV	YPE:	inte	erna.	1							
60		(xi)	SE	QUEN	CE DI	ESCR	IPTIC	ON:	SEQ :	ID N	0:62	:				
00	Gly 1	Ala	Thr	Arg	Asp 5	Arg	Pro	Leu	Trp	Ile 10	Ile	Phe	Ser	Gly	Asn 15	Met
65	Asn	Ile	Lys	Leu 20	Lys	Met	Pro	Met	Tyr 25	Ile	Ala	Gly	Tyr	Lys 30	Thr	Phe
	Asp	Gly	Arg 35	Gly	Ala	Gln	Val	Tyr 40	Ile	Gly	Asn	Gly	Gly 45	Pro	Cys	Val
70	Phe	Ile 50	Lys	Arg	Val	Ser	Asn 55	Val	Ile	Ile	His	Gly 60				
	(2)	INFO	RMA	TON	FOR	SEO	TO	VO : 61	3 •							



5		(1)	(Z	A) LI 3) T	ENGTI	H: 50 amir DGY:	ami	ino a cid		3						
		(ii)	MOI	LECUI	LE T	YPE:	pept	ide								
10						YPE: ESCRI				ID NO	0:63	:				
15	Leu 1	Gly		_									Glu	Pro	Val 15	His
15	Pro	Gln	Asp	Gly 20	Asp	Ala	Leu	Thr	Leu 25	Arg	Thr	Ala	Thr	Asn 30	Ile	Trp
20	Ile	Asp	His 35	Asn	Ser	Phe	Ser	Asn 40	Ser	Ser	Asp	Gly	Leu 45	Val	Asp	Val
	Thr	Leu 50														
25	(2)	INFO	RMAT	NOI	FOR	SEQ	ID 1	10:64	1:							
30		(i)	(Z	A) LI B) TY	ENGTI	HARAC H: 90 amir DGY:) ami	ino a cid		6						
		(ii)	MOI	LECUI	LE T	PE:	pept	ide								
35		(v)	FR?	AGMEN	T T!	PE:	inte	erna]	L							
		(xi)	SEÇ	QUENC	CE DI	ESCRI	PTIC	ON: S	SEQ]	ID NO	64:	:				
40	1	Phe			5					10					15	
	Tyr	Ser	Asp	Asp 20	Lys	Ser	Met	Lys	Val 25	Thr	Val	Ala	Phe	Asn 30	Gln	Phe
45	Gly	Pro	Asn 35	Cys	Gly	Gln	Arg	Met. 40	Pro	Arg	Ala	Arg	Tyr 45	Gly	Leu	Val
	His	Val 50	Ala	Asn	Asn	Asn	Tyr 55	Asp	Pro	Trp	Thr	Ile 60	Tyr	Ala	Ile	Gly
50	Gly 65	Ser	Ser	Asn	Pro	Thr 70	Ile	Leu	Ser	Glu	Gly 75	Asn	Ser	Phe	Thr	Ala 80
	Pro	Asn	Glu	Ser	Tyr 85		Lys	Gln	Val	Thr 90						
55	(2)	INFO	RMAT	NOI	FOR	SEQ	ID N	10:65	5:							
60		(i)	(Ž	Ã) LE 3) TY	ENGTI	HARAC H: 63 amir OGY:	ami	no a		5						
		(ii)	MOI	LECUI	E T	PE:	pept	iđe								
65		(v)	FRA	AGMEN	T T!	PE:	inte	ernal	L							
		(xi)	SEÇ	QUENC	E DE	ESCRI	PTIC	N: S	SEQ I	D NO	:65	:				





	Cys	Ser	Asn	Trp	Val	Trp	Gln	Ser	Thr		Asp	Val	Phe	Tyr		Gly
5	Ala	Tyr	Phe	Val 20	Ser	Ser	Gly	Lys	Tyr 25	Glu	Gly	Gly	Asn	Ile 30	15 Tyr	Thr
	Lys	Lys	Glu 35	Ala	Phe	Asn	Val	Glu 40	Asn	Gly	Asn	Ala	Thr 45	Pro	Gln	Leu
10	Thr	Lys 50	Asn	Ala	Gly	Val	Leu 55	Thr	Cys	Ser	Leu	Ser 60	Lys	Arg	Cys	
	(2)	INF	ORMAT	NOIT	FOR	SEQ	ID 1	NO:6	5:							
15		(i)	(<i>I</i>	3) TY	ENGTI (PE:	1: 50 amin		ino a cid	CS: acids	3						
20		(ii)	MOI	LECUI	E T	PE:	pept	ide								
		(v)	FRA	AGMEN	1T T	PE:	inte	erna:	1							
2.5		(xi)	SEÇ	QUENC	E DE	ESCR	IPTIC	ON: S	SEQ :	ID NO	:66	:				
25	Asp 1	Asn	Pro	Ile	Asp 5	Ser	Cys	Trp	Arg	Gly 10	Asp	Ser	Asn	Trp	Ala 15	Gln
30	Asn	Arg	Met	Lys 20	Asp	Ser	Asn	Trp	Ala 25	Gln	Asn	Arg	Met	Lys 30	Leu	Ala
	Asp	Cys	Ala 35	Val	Gly	Phe	Gly	Ser 40	Ser	Thr	Met	Gly	Gly 45	Lys	Gly	Gly
35	Asp	Leu 50														
	(2)	INFO	RMAT	NOIT	FOR	SEQ	ID N	10:67	7:							
40		(i)	. =	3) TY	ENGTI	H: 30 amir		ino a cid	CS: acids	5						
45		(ii)	MOI	ECUI	E TY	PE:	pept	ide								
		(v)	FRA	GMEN	1T TY	PE:	inte	ernal	L							
50		(xi)	SEÇ	QUENC	E DE	ESCRI	PTIC	ON: S	SEQ]	D NO	:67:	:				
50	Lys 1	Met	Pro	Met	Tyr 5	Ile	Ala	Gly	Tyr	Lys 10	Thr	Phe	Asp	Gln	Arg 15	Gly
55	Ala	Gln	Val	Tyr 20	Ile	Gly	Asn	Gly	Gly 25	Pro	Cys	Val	Phe	Ile 30		
	(2)	INFO	RMAT	NOI	FOR	SEQ	ID N	10:68	3:							
60		(i)	(<i>P</i>	QUENC A) LE B) TY O) TO	NGTH PE:	I: 30 amir) ami 10 ac	ino a	CS: acids	5						
65		(ii)	MOL	ECUL	ΈΤΥ	PE:	pept	ide								
O)		(v)	FRA	AGMEN	TY	PE:	inte	ernal	L							
		(xi)	SEÇ	UENC	E DE	SCRI	PTIC	N: S	SEQ 1	D NO	:68:					





	Asp 1	Ala	Leu	Thr	Leu 5	Arg	Thr	Ala	Thr	Asn 10	Ile	Trp	Ile	Asp	His 15	Asn
5	Ser	Phe	Ser	Asn 20	Ser	Ser	Asp	Gly	Leu 25	Val	Asp	Val	Thr	Leu 30		
	(2)	INFO	RMAT	NOI	FOR	SEQ	ID 1	۷O: 69	:							
10		(i)						ISTIC ino a		3						
			(E				no ao line									
15		(ii)	MOI	LECUI	E T	YPE:	pept	cide								
		(v)	FRA	AGMEN	T T!	YPE:	inte	erna:	L							
20		(xi)	SEÇ	QUENC	E DI	ESCR	IPTIC	on: s	SEQ I	ID NO	69:	:				
20	Leu 1	Phe	Phe	Asn	His 5	His	Lys	Val	Met	Leu 10	Leu	Gly	His	Asp	Asp 15	Ala
25	Tyr	Ser .	Asp	Asp 20	Lys	Ser	Met	Lys	Val 25	Thr	Val	Ala	Phe	Asn 30	Gln	Phe
	Gly	Pro .	Asn 35	Cys	Gly	Gln	Arg	Met 40	Pro	Arg	Ala	Arg	Tyr 45	Gly	Leu	Val
30	His	Val 50														
	(2)	INFO	RMAT	NOI	FOR	SEQ	ID 1	vo:70):							
35		(i)	(Z	A) LE	ENGTI PE:	H: 40 amir	_			5						
40		(ii)	MOI	ECUI	E TY	PE:	pept	ide								
		(v)	FRA	AGMEN	T TY	PE:	inte	ernal	L							
45		(xi)	SEÇ	QUENC	E DE	ESCR	PTIC	ON: S	SEQ]	D NO	70:70					
.5	Cys 1	Ser .	Asn	Trp	Val 5	Trp	Gln	Ser	Thr	Gln 10	Asp	Val	Phe	Tyr	Asn 15	Gly
50	Ala	Tyr	Phe	Val 20	Ser	Ser	Gly	Lys	Tyr 25	Glu	Gly	Gly	Asn	Ile 30	Tyr	Thr
	Lys	Lys (Glu 35	Ala	Phe	Asn	Va1	Glu 40								
55	(2)	INFO	RMAT	NOI	FOR	SEQ	ID I	10:72	L:							
60		(i)	(A	A) LE 3) TY	NGTH	4: 30 amir				5						
		(ii)														
65		(v)	FRA	AGMEN	T TI	PE:	inte	erna:	L							





		(71)	SEQU) EI/(L	e De.	SCRI	PITOI	N: 51	rQ II) NO	:/1:						
_		Lys 1	Met	Pro	Met	Tyr 5	Ile	Ala	Gly	Tyr	Lys 10	Thr	Phe	Asp	Gly	Arg 15	Gly
5		Ala	Gln	Val	Tyr 20	Ile	Gly	Asn	Gly	Gly 25	Pro	Cys	Val	Phe	Ile 30		
10	(2)	INFO	RMAT	ION I	FOR :	SEQ :	ID NO	72:72	:								
15		(i)	(A) (B) (D)	JENCI) LEI) TYI) TOI	NGTH PE: 6 POLO	: 24 amin GY:	amin o ac: linea	no ao id ar									
IJ		(ii)	FRAG			_											
		(xi)		JENCI					EO TI	OM C	.72.						
20												Asp	Glv	Ara	Gly	Ala	Gln
		1		-2 -		5	1	-2-	-1		10		2	9	2	15	
25		Val	Tyr	Ile	Gly 20	Asn	Gly	Gly	Pro								
	(2)	INFO	RMAT	ION I	FOR :	SEQ :	ID NO	73:73	:								
30		(i)	(A)	JENCI) LEI) TYI) TOI	NGTH PE: 6	: 22 amin	amir o ac:	no ao id									
35		(ii)	MOLI	ECULI	E TY	PE:]	pept	ide									
,,		(v)	FRAC	GMENT	r TY	PE:	inte	rnal									
		(xi)	SEQU	JENCI	E DE	SCRI	OIT	N: SI	EQ II	ои о	:73:						
40		Tyr 1	Ile	Ala	Gly	Tyr 5	Lys	Thr	Phe	Asp	Gly 10	Arg	Gly	Ala	Gln	Val 15	Tyr
45		Ile	Gly	Asn	Gly 20	Gly	Pro										
•5	(2)	INFO	RMAT:	ION I	FOR :	SEQ :	ID NO	74	:								
50		(i)	(B)	JENCI) LEI) TYI) TOI	NGTH PE: 8	: 24 amin	amin o ac:	no ao id									
		(ii)	MOLI	ECULI	E TY	PE:]	pept:	ide									
55		(v)	FRAC	GMENT	r TY	PE:	inte	rnal									
		(xi)	SEQU	JENCI	E DE:	SCRI	OIT	V: S	EQ II	ОИО	:74:						
50		Lys 1	Lys	Tyr	Ile	Ala 5	·Gly	Tyr	Lys	Thr	Phe 10	Asp	Gly	Arg	Gly	Ala 15	Gln
		Val	Tyr	Ile	Gly 20	Asn	Gly	Gly	Pro								
55	(2)	INFO	RMAT:	ION E	FOR S	SEQ :	ID NO	0:75	:								





5		(1)	(A) LENGTH: 30 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear
		(ii)	MOLECULE TYPE: peptide
		(v)	FRAGMENT TYPE: internal
10		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:75:
15		Asp 1	Ala Leu Thr Leu Arg Thr Ala Thr Asn Ile Trp Ile Asp His Asn 10 15
13		Ser	Phe Ser Asn Ser Ser Asp Gly Leu Val Asp Val Thr Leu 20 25 30
20	(2)	INFO	RMATION FOR SEQ ID NO:76:
		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear
25		(ii)	MOLECULE TYPE: peptide
		(v)	FRAGMENT TYPE: internal
30		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:76:
		Arg 1	Thr Ala Thr Asn Ile Trp Ile Asp His Asn Ser Phe Ser Asn Ser 5 10 15
35		Ser	Asp Gly Leu Val Asp 20
	(2)	INFO	RMATION FOR SEQ ID NO:77:
40		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear
45		(ii)	MOLECULE TYPE: peptide
		(v)	FRAGMENT TYPE: internal
50		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:77:
50		Lys 1	Arg Thr Ala Thr Asn Ile Trp Ile Asp His Asn Ser Phe Ser Asn 5 10 15
55		Ser	Ser Asp Gly Leu Val Asp Lys 20
	(2)	INFO	RMATION FOR SEQ ID NO:78:
60			SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear
			MOLECULE TYPE: peptide
65		(V)	FRAGMENT TYPE: internal



4		
•	-	

		(XI)	SEQU	ENCE	s DES	SCRI.	P.1.1OI	N: SI	₹Ö TI	ON C	:/8:						
5		Lys 1	Ser	Met	Lys	Val 5	Thr	Val	Ala	Phe	Asn 10	Gln	Phe	Gly	Pro	Asn 15	Сув
J		Gly	Gln	Arg	Met 20	Pro	Arg	Ala	Arg	Tyr 25	Gly	Leu	Val	His	Val 30	Ala	Asn
10		Asn	Asn	Tyr 35	Asp												
	(2)	INFO	RMATI	ON F	FOR S	SEQ :	ID N	0:79	:								
15		(i)	(B)	LEN TYE	NGTH PE: a	: 30 amin		no ao id									
20		(ii)	MOLE	CULE	TYI	PE: 1	pept:	ide									
20		(v)	FRAG	MENT	וצד ז	PE: :	inte	rnal									
		(xi)	SEQU	ENCE	E DES	SCRI	PTIO	N: SI	EQ II	ои с	:79						
25		Lys 1	Ser	Met	Lys	Val 5	Thr	Val	Ala	Phe	Asn 10	Gln	Phe	Gly	Pro	Asn 15	Cys
30		Gly	Gln	Arg	Met 20	Pro	Arg	Ala	Arg	Tyr 25	Gly	Leu	Val	His	Val 30		
<i>.</i>	(2)	INFO	RMATI	ON F	FOR S	SEQ :	ID N	08:0	•								
35		(i)	~	LEN TYF	IGTH:	: 30 amin		no ao id									
		(ii)	MOLE	CULE	TYI	PE: 1	pept	ide									
40		(v)	FRAG	MENT	TYI	PE: :	inte	rnal									
		(xi)	SEQU	ENCE	E DES	SCRII	OITS	N: SI	EQ II	ои с	:80:						
45		Lys 1	Ser	Met	Lys	Val 5	Thr	Val	Ala	Phe	Asn 10	Gln	Phe	Gly	Pro	Asn 15	Ser
		Gly	Gln	Arg	Met 20	Pro	Arg	Ala	Arg	Tyr 25	Gly	Leu	Val	His	Val 30		
50	(2)	INFO	RMATI	ON F	OR S	SEQ I	ID NO	81:	:								
		(i)	SEQU (A)					STICS no ac									
55			(B) (D)				o aci Linea										
		(ii)	MOLE	CULE	TYF	PE: p	pept	ide									
50		(v)	FRAG	MENT	TYE	PE: :	intei	nal									
		(xi)	SEQU	ENCE	DES	SCRIE	OITS	V: SE	EQ II	ON C	:81:						
65		Lys 1	Ser	Met	Lys	Val 5	Thr	Val	Ala	Phe	Asn 10	Gln	Phe	Gly	Pro	Asn 15	Cys





Gly Gln Arg Met Pro Arg Ala Arg Tyr Gly Leu Val 20 25

(2) INFORMATION FOR SEQ ID NO:82: 5 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear 10 (ii) MOLECULE TYPE: peptide (v) FRAGMENT TYPE: internal 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82: Lys Ser Met Lys Val Thr Val Ala Phe Asn Gln Phe Gly Pro Asn Cys 20 Gly Gln Arg Met Pro Arg Ala Arg Tyr Gly Leu Val (2) INFORMATION FOR SEQ ID NO:83: 25 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear 30 (ii) MOLECULE TYPE: peptide (v) FRAGMENT TYPE: internal (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83: 35`~ Lys Ser Met Lys Val Thr Val Ala Phe Asn Gln Phe Gly Pro Asn Cys Gly Gln Arg Met Pro Arg Ala Arg Tyr Gly 40 25 (2) INFORMATION FOR SEQ ID NO:84: (i) SEQUENCE CHARACTERISTICS: 45 (A) LENGTH: 26 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear 50 (ii) MOLECULE TYPE: peptide (v) FRAGMENT TYPE: internal (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84: 55 Lys Ser Met Lys Val Thr Val Ala Phe Asn Gln Phe Gly Pro Asn Ser 5 15 Gly Gln Arg Met Pro Arg Ala Arg Tyr Gly 60 (2) INFORMATION FOR SEQ ID NO:85: (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid





			(D) TOPOL	OGY:	linea	ar									
		(ii)	MOLECULE T	YPE:	pepti	de									
5		(v)	FRAGMENT I	YPE:	inter	nal									
		(xi)	SEQUENCE D	ESCRI	PTION	l: SE	EQ II	ON C	85:						
10		Lys 1	Ser Met Ly	s Val	Thr	Val	Ala	Phe	Asn 10	Gln	Phe	Gly	Pro	Asn 15 .	Ser
		Gly	Gln Arg Me		Arg	Ala	Arg	Tyr 25	Gly	Lys	Lys				
15	(2)	INFO	RMATION FOR	SEQ	ID NO	86:	:								
20	· .	(i)	SEQUENCE C (A) LENGT (B) TYPE: (D) TOPOL	H: 26 amin	amir o aci	no ac .d									
		(ii)	MOLECULE I	YPE:	pepti	.de									
25	*	(v)	FRAGMENT T	YPE:	inter	nal									
25		(xi)	SEQUENCE D	ESCRI	PTION	l: SE	EQ II	ON C	86:						
30	·	Lys 1	Ser Met Ly	s Val 5	Thr	Val	Aļa	Phe	Asn 10	Gln	Phe	Gly	Pro	Asn 15	Cys
	į.	Gly	Gln Arg Me 20		Arg	Ala	Arg	Tyr 25	Gly					,	
35	(2)	INFO	RMATION FOR	SEQ	ID NO	87:	:								
<i>33</i>		(i)	SEQUENCE C (A) LENGT												
40	,		(B) TYPE: (D) TOPOL	amin OGY:											
		(ii)	MOLECULE T	YPE:	pepti	.de									
45		(v)	FRAGMENT T	YPE:	inter	nal									
7,7		(xi)	SEQUENCE D	ESCRI	PTION	l: SE	EQ II	NO:	87:		,				
50		Pro 1	Arg Ala Ar	g Tyr 5	Gly	Leu	Val	His	Val 10	Ala	Asn	Asn	Asn	Tyr 15	Asp
50		Pro	Trp Thr Il		Ala	Ile	Gly	Gly 25	Ser	Ser	Asn	Pro	Thr 30		
55	(2)	INFO	MATION FOR	SEQ	ID NO	:88:	:								
		(i)	SEQUENCE C (A) LENGT (B) TYPE: (D) TOPOL	H: 28 amin	amin o aci	no ac .d									
60		(ii)	MOLECULE T	YPE:	pepti	.de									
		(v)	FRAGMENT T	YPE:	inter	nal									

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:





		Arg 1	Ala Ai	g Tyr	Gly 5	Leu	Val	His	Val	Ala 10	Asn	Asn	Asn	Tyr	Asp 15	Pro
5		Trp	Thr I	le Tyr 20	Ala	Ile	Gly	Gly	Ser 25	Ser	Asn	Pro				
	(2)	INFOR	MATION	1 FOR	SEQ :	ID N	0:89	:								
10		(i)	(B) T	ICE CH LENGTH TYPE: TOPOLO	: 26 amin	amino ac:	no ao id									
15		(ii) 1	MOLECU	JLE TY	PE:]	pept:	ide									
15		(v)	FRAGMI	ENT TY	PE:	inte	rnal									
		(xi)	SEQUE	ICE DE	SCRI	PTIO	N: S1	EQ II	D NO	:89:						
20		Arg . 1	Ala Ai	rg Tyr	Gly 5	Leu	Val	His	Val	Ala 10	Asn	Asn	Asn	Tyr	Asp 15	Pro
25		Trp	Thr I	le Tyr 20	Ala	Ile	Gly	Gly	Ser 25	Ser						
23	(2)	INFOR	MATION	1 FOR	SEQ :	ID N	0:90	:								
30		(i)	SEQUEN (A) I	ICE CH LENGTH									-			•
				TYPE: TOPOLO												
35		(ii) 1	MOLECU	JLE TY	PE:]	pept:	ide									
		(v)	FRAGME	ENT TY	PE:	inte	rnal									
		(xi)	SEQUEN	ICE DE	SCRI	OITG	N: SI	EQ II	D NO	:90:						
40		Asp	Val Ph	ne Tyr	Asn 5	Gly	Ala	Tyr	Phe	Val 10	Ser	Ser	Gly	Lys	Tyr 15	Glu
45		Gly	Gly As	sn Ile 20	Tyr	Thr	Lys	Lys	Glu 25	Ala	Phe	Asn	Val	Glu 30		
	(2)	INFOR	MOITAM	1 FOR	SEQ :	ID N	0:91	:								
50		(i)	(B) 7	ICE CH LENGTH TYPE: TOPOLO	: 26 amin	amin ac:	no ao id									
		(ii) 1	MOLECU	JLE TY	PE:]	pept:	ide									
55		(v)	FRAGMI	ENT TY	PE:	inte	rnal									
		(xi)	SEQUE	ICE DE	SCRI	PTIOI	N: SI	EQ II	D NO	:91:						
60		Asn (Gly Al	.a Tyr	Phe 5	Val	Ser	Ser	Gly	Lys 10	Tyr	Glu	Gly	Gly	Asn 15	Ile
		Tyr	Thr Ly	rs Lys 20	Glu	Ala	Phe	Asn	Val 25	Glu						
65	(2)	INFOR	MATION	FOR	SEQ :	ID NO	0:92	:								



	_
•	

5	(1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	
J	(ii) MOLECULE TYPE: peptide	
	(v) FRAGMENT TYPE: internal	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:	
	Asn Gly Ala Tyr Phe Val Ser Ser Gly Lys Tyr Glu Gly Gly Asn Ile 1 5 10 15	
15	Tyr Thr Lys Lys Glu Ala Phe Asn 20	
	(2) INFORMATION FOR SEQ ID NO:93:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 amino acids	
25	(B) TYPE: amino acid (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: peptide	
	(v) FRAGMENT TYPE: internal	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:	
	Lys Lys Asn Gly Ala Tyr Phe Val Ser Ser Gly Lys Tyr Glu Gly Gly 1 5 10 15	
35	Asn Ile Tyr Thr Lys Lys Glu Ala Phe Asn 20 25	
	(2) INFORMATION FOR SEQ ID NO:94:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1170 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
45	(ii) MOLECULE TYPE: cDNA	
50	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 261126	
55	<pre>(ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION: 891126</pre>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:	
60	AAATTCTATA TTCTGAACCC TAAAA ATG GCT TCC CCA TGC TTA ATA GCA GTC Met Ala Ser Pro Cys Leu Ile Ala Val -21 -20 -15	52
65	CTT GTT TTC CTT TGT GCA ATT GTA TCT TGT TAC TCT GAT AAT CCC ATC Leu Val Phe Leu Cys Ala Ile Val Ser Cys Tyr Ser Asp Asn Pro Ile -10 -5 1	00



	·	
GAC AGC TGC TGG AGA GGA GAT TCG Asp Ser Cys Trp Arg Gly Asp Ser 5 10	AAC TGG GAT CAA AAC AGA ATG AAG Asn Trp Asp Gln Asn Arg Met Lys 15 20	
5 CTC GCA GAC TGT GCT GTG GGA TTT Leu Ala Asp Cys Ala Val Gly Phe 25	GGA AGC TCC ACC ATG GGA GGC AAA 196 Gly Ser Ser Thr Met Gly Gly Lys 30 35	
GGA GGA GAT TTT TAC ACC GTC ACA Gly Gly Asp Phe Tyr Thr Val Thr 40	AGC ACA GAT GAT AAT CCT GTG AAT Ser Thr Asp Asp Asn Pro Val Asn 45 50	
CCT ACA CCA GGA ACT TTG CGC TAT Pro Thr Pro Gly Thr Leu Arg Tyr 55 60		
TGG ATC ATT TTC TCT CAG AAT ATG Trp Ile Ile Phe Ser Gln Asn Met 70 75	AAT ATA AAG CTC AAG ATG CCT TTG 340 Asn Ile Lys Leu Lys Met Pro Leu 80	
TAT GTT GCT GGA CAT AAG ACT ATT Tyr Val Ala Gly His Lys Thr Ile 85 90	GAC GGC AGG GGA GCA GAT GTT CAT Asp Gly Arg Gly Ala Asp Val His 95 100	
25 CTT GGC AAC GGC GGT CCC TGT CTG Leu Gly Asn Gly Gly Pro Cys Leu 105	TTT ATG AGG AAA GTG AGC CAT GTT 436 Phe Met Arg Lys Val Ser His Val 110 115	
ATT CTC CAT AGT TTG CAT ATA CAC Ile Leu His Ser Leu His Ile His 120		
GAT GTT TTG GTA AGT GAG TCT ATT Asp Val Leu Val Ser Glu Ser Ile 135 140	GGG GTC GAG CCT GTT CAT GCT CAG Gly Val Glu Pro Val His Ala Gln 145	
GAT GGG GAC GCC ATT ACT ATG CGC Asp Gly Asp Ala Ile Thr Met Arg 150 155	CAT GTT ACA AAT GCT TGG ATT GAT His Val Thr Asn Ala Trp Ile Asp 160	
CAT AAT TCT CTC TCC GAT TGT TCT His Asn Ser Leu Ser Asp Cys Ser 165		
GGC TCC ACT GGA ATT ACT ATC TCC Gly Ser Thr Gly Ile Thr Ile Ser 185	AAC AAT CAC TTC TTC AAC CAT CAT Asn Asn His Phe Phe Asn His His 190 195	
AAA GTG ATG TTA TTA GGA CAT GAT Lys Val Met Leu Leu Gly His Asp 200		
ATG AAA GTG ACA GTG GCG TTC AAT Met Lys Val Thr Val Ala Phe Asn 215 220		
AGA ATG CCA AGG GCA CGA TAT GGA Arg Met Pro Arg Ala Arg Tyr Gly 230 235		
TAT GAT CCA TGG AAT ATA TAT GCT . Tyr Asp Pro Trp Asn Ile Tyr Ala 245 250		



	ATT CTG Ile Leu													916
5	AAG CAA Lys Gln	Val T												964
10	AAC TGG Asn Trp					g Asp								1012
15	TTT GTA Phe Val 310	Ser Se		Lys 7										1060
20	GAA GCT Glu Ala 325													1108
•	AAT GCT Asn Ala				FAAGCT(CTCT (CTAAZ	ATCTT	rg c	TATC	GAAA	2		1156
25	GAAAAAA	TAT AT	AG											1170
	(2) INF			SEO I	ID NO:	95:								
30	(4, 2010		QUENCE				•							
			(A) LE1 (B) TYI (D) TOI	NGTH: PE: an	367 au mino a	mino a		3						
35	(ii) MOI	LECULE	TYPE:	: prot	ein								
	(xi) SE	QUENCE	DESCE	RIPTIO	N: SE	Q ID	NO:9	95:					
40	Met Ala -21 -20		ro Cys		Ile Ala -15	a Val	Leu	Val	Phe -10	Leu	Cys	Ala	Ile	
	Val Ser -5	Суз Ту	yr Ser	Asp A	Asn Pro	o Ile	Asp 5	Ser	Cys	Trp	Arg	Gly 10	Asp	
45	Ser Asn	Trp As	sp Gln 15	Asn A	Arg Me	Lys 20	Leu	Ala	Asp	Cys	Ala 25	Val	Gly	
50	Phe Gly	Ser Se	er Thr	Met 0	Gly Gly	_	Gly	Gly	Asp	Phe 40	Tyr	Thr	Val	
30	Thr Ser		sp Asp	Asn E	Pro Vai	l Asn	Pro	Thr	Pro 55	Gly	Thr	Leu	Arg	
55	Tyr Gly 60	Ala T	hr Arg	Glu I 65	Lys Ala	a Leu	Trp	11e 70	Ile	Phe	Ser	Gln	Asn 75	
	Met Asn	Ile Ly	ys Leu 80	Lys N	Met Pro) Leu	Tyr 85	Val	Ala	Gly	His	Lys 90	Thr	
60	Ile Asp		rg Gly 95	Ala A	Asp Va	l His 100	Leu	Gly	Asn	Gly	Gly 105	Pro	Cys	
	Leu Phe	Met A	rg Lys	Val S	Ser Hi	s Val	Ile	Leu	His	Ser	Leu	His	Ile	





	1115	125	СуЗ	Vell	1111	SET	130	цеu	Gly	АБР	vai	135	vai	ser	GIU	ser	
5	Ile 140	Gly	Val	Glu	Pro	Val 145		Ala	Gln	Asp	Gly 150	Asp	Ala	Ile	Thr	Met 155	
,	Arg	His	Val	Thr	Asn 160	Ala	Trp	Ile	Asp	His 165	Asn	Ser	Leu	Ser	Asp 170	Cys	
10	Ser	Asp	Gly	Leu 175	Ile	Asp	Val	Thr	Leu 180	Gly	Ser	Thr	Gly	Ile 185	Thr	Ile	
	Ser	Asn	Asn 190	His	Phe	Phe	Asn	His 195	His	Lys	Val	Met	Leu 200	Leu	Gly	His	
15	Asp	Asp 205	Thr	Tyr	Asp	Asp	Asp 210	Lys	Ser	Met	Lys	Val 215	Thr	Val	Ala	Phe	
20	Asn 220	Gln	Phe	Gly	Pro	Asn 225	Ala	Gly	Gln	Arg	Met 230	Pro	Arg	Ala	Arg	Tyr 235	
	Gly	Leu	Val	His	Val 240	Ala	Asn	Asn	Asn	Tyr 245	Asp	Pro	Trp	Asn	Ile 250	Tyr	
25	Ala	Ile	Gly	Gly 255	Ser	Ser	Asn	Pro	Thr 260	Ile	Leu	Ser	Glu	G1y 265	Asn	Ser	
	Pĥe	Thr	Ala 270	Pro	Ser	Glu	Ser	Tyr 275	Lys	Lys	Gln	Val	Thr 280	Lys	Arg	Ile	
30	Gly	Cys 285	Glu	Ser	Pro	Ser	Ala 290	Cys	Ala	Asn	Trp	Val 295	Trp	Arg	Ser	Thr	
35	Arg 300	Asp	Ala	Phe	Ile	Asn 305	Gly	Ala	Tyr	Phe	Val 310	Ser	Ser	Gly	Lys	Thr 315	
33	Glu	Glu	Thr	Asn	Ile 320	Tyr	Asn	Ser	Asn	Glu 325	Ala	Phe	Lys	Val	Glu 330	Asn	
40	Gly	Asn	Ala	Ala 335	Pro	Gln	Leu	Thr	Lys 340	Asn	Ala	Gly	Val	Val 345	Thr		
	(2)					SEQ											
45		(1)	() () ()	A) LI 3) T' C) S'	ENGTI PE: PRANI	HARACH: 12 nucl DEDNI DGY:	278 l Leic ESS:	ase acio sino	pai:	rs							
50		(ii)) MOI	LECUI	LE T	YPE:	CDN	A									
55		(ix)	(2	•	AME/I	KEY:		.1145	5								
33		(ix)	(2		AME/I	KEY:											
60		(xi)) SE(QUENC	CE DI	ESCR	[PTIC	on: S	SEQ :	ID NO	96:	:					
	CGG'	ratac	GAT A	AGAT:	rcta:	ra To	rctg?	AGCC	TA				rcc (Ser 1				53
65											-21 -		4		-,		





	ATA Ile -15	GCA Ala	TTC Phe	CTT Leu	GTT Val	TTC Phe -10	CTT Leu	TGT Cys	GCA Ala	ATT Ile	GTA Val -5	TCT Ser	TGT Cys	TGC Cys	TCT Ser	GAT Asp 1	101
5	AAT Asn	CCC Pro	ATA Ile	GAC Asp 5	AGC Ser	TGC Cys	TGG Trp	AGA Arg	GGA Gly 10	GAT Asp	TCG Ser	AAC Asn	TGG Trp	GGT Gly 15	CAA Gln	AAC Asn	149
10	AGA Arg	ATG Met	AAG Lys 20	CTC Leu	GCA Ala	GAT Asp	TGC Cys	GCT Ala 25	GTG Val	GGA Gly	TTT Phe	GGA Gly	AGC Ser 30	TCC Ser	ACC Thr	ATG Met	197
15	GGA Gly	GGC Gly 35	AAA Lys	GGA Gly	GGA Gly	GAT Asp	TTT Phe 40	TAC Tyr	ACC Thr	GTC Val	ACA Thr	AGC Ser 45	GCA Ala	GAT Asp	GAT Asp	AAT Asn	245
20		GTG Val															293
20	AAA Lys	GCA Ala	CTT Leu	TGG Trp	ATC Ile 70	ATT Ile	TTC Phe	TCT Ser	CAG Gln	AAT Asn 75	ATG Met	AAT Asn	ATA Ile	AAG Lys	CTC Leu 80	AAG Lys	341
25	ATG Met	CCT Pro	TTG Leu	TAT Tyr 85	GTT Val	GCT Ala	GGA Gly	CAT His	AAG Lys 90	ACT Thr	ATT Ile	GAC Asp	GGC Gly	AGG Arg 95	GGA Gly	GCA Ala	389
30	GAT Asp	GTT Val	CAT His 100	CTT Leu	GGC Gly	AAC Asn	GGC Gly	GGT Gly 105	CCC Pro	TGT Cys	CTG Leu	TTT Phe	ATG Met 110	AGG Arg	AAA Lys	GTG Val	437
35	AGC Ser	CAT His 115	GTT Val	ATT Ile	CTC Leu	CAT His	GGT Gly 120	TTG Leu	CAT His	ATA Ile	CAC His	GGT Gly 125	TGT Cys	AAT Asn	ACT Thr	AGT Ser	485
40		TTG Leu															533
10		CCC Pro															581
45		GTC Val															629
50	GTT Val	ACT Thr	CTT Leu 180	GCT Ala	TCC Ser	ACT Thr	GCT Ala	GTT Val 185	ACT Thr	ATT Ile	TCC Ser	AAT Asn	AAC Asn 190	CAC His	TTC Phe	TTC Phe	677
55	GAC Asp	CAT His 195	GAT Asp	GAA Glu	GTG Val	ATG Met	TTG Leu 200	TTA Leu	GGA Gly	CAT His	AGT Ser	GAT Asp 205	TCA Ser	TTC Phe	TCA Ser	GAT Asp	725
60		AAA Lys															773
50		GTG Val															821



	025.5US.AP
AAT AAT AAT TAT GAG CCA TGG GGA AAA TAT GCC ATT GGA GGA AGT TCT Asn Asn Asn Tyr Glu Pro Trp Gly Lys Tyr Ala Ile Gly Gly Ser Ser 245 250 255	869
GAT CCA ACA ATT ATA AGT GAA GGG AAT AGA TTT CTT GCA CCA AAT GAA Asp Pro Thr Ile Ile Ser Glu Gly Asn Arg Phe Leu Ala Pro Asn Glu 260 265 270	917
TCT TAT AAA AAG GAG GTG ACA ATA CGT GTA GGT TGT AAA TCT ACA AGT Ser Tyr Lys Lys Glu Val Thr Ile Arg Val Gly Cys Lys Ser Thr Ser 275 280 285	965
TGT GAT GCA TGG GAG TGG AGA TCA AAA GAT GAT GCC TTC CTT AAT GGT Cys Asp Ala Trp Glu Trp Arg Ser Lys Asp Asp Ala Phe Leu Asn Gly 290 295 300 305	1013
GCC TAT TTT GTA CAA TCA GGC AAG GGG TAT AAT GGT GGA GAG GCA TTC Ala Tyr Phe Val Gln Ser Gly Lys Gly Tyr Asn Gly Gly Glu Ala Phe 310 315 320	1061
AAG GTT GAA AGT GCA AAT GAG GTG CCA ACA TTG ACT AAA CAT GCT GGA Lys Val Glu Ser Ala Asn Glu Val Pro Thr Leu Thr Lys His Ala Gly 325 330 335	1109
GCA TTA AAA TGT ATA CCT ACC AAA CAA TGT GTG ATA TGAAAAGTCA Ala Leu Lys Cys Ile Pro Thr Lys Gln Cys Val Ile 340 345	1155
ATCGATATAA TAATGTGTTA TTTGTAATAT TTCAGCTTTG AATATGTATA GAAAAAGAAT	1215
TTCAACAAAA TGACACTATT ATATAAATAA ATTCTTAGTT TATTAGTTGG TATTAAAAAA	1275
AAA	1278
(2) INFORMATION FOR SEQ ID NO:97:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 370 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: protein	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:	
Met Ala Ser Pro Cys Leu Ile Ala Phe Leu Val Phe Leu Cys Ala Ile -21 -2015 -10	
Val Ser Cys Cys Ser Asp Asn Pro Ile Asp Ser Cys Trp Arg Gly Asp -5 10	
Ser Asn Trp Gly Gln Asn Arg Met Lys Leu Ala Asp Cys Ala Val Gly	

Phe Gly Ser Ser Thr Met Gly Gly Lys Gly Gly Asp Phe Tyr Thr Val $_{\rm 30}$ $_{\rm 35}$ $_{\rm 40}$

Thr Ser Ala Asp Asp Asn Pro Val Asn Pro Thr Pro Gly Thr Leu Arg
45 50 55

Tyr Gly Ala Thr Arg Glu Lys Ala Leu Trp Ile Ile Phe Ser Gln Asn 60 65 70 75

Met Asn Ile Lys Leu Lys Met Pro Leu Tyr Val Ala Gly His Lys Thr 80 85 90





	Ile	Asp	Gly	Arg 95	Gly	Ala	Asp	Val	His 100	Leu	Gly	Asn	Gly	Gly 105	Pro	Cys
5	Leu	Phe	Met 110	Arg	Lys	Val	Ser	His 115	Val	Ile	Leu	His	Gly 120	Leu	His	Ile
	His	Gly 125	Cys	Asn	Thr	Ser	Val 130	Leu	Gly	Asp	Val	Leu 135	Val	Ser	Glu	Ser
10	Ile 140	Gly	Val	Val	Pro	Val 145	His	Pro	Gln	Asp	Gly 150	Asp	Ala	Phe	Thr	Val 155
	Arg	Thr	Ser	Glu	His 160	Ile	Trp	Val	Asp	His 165	Asn	Thr	Leu	Ser	Asn 170	Gly
15	Thr	Asp	Gly	Leu 175	Val	Asp	Val	Thr	Leu 180	Ala	Ser	Thr	Ala	Val 185	Thr	Ile
20	Ser	Asn	Asn 190	His	Phe	Phe	Asp	His 195	Asp	Glu	Val	Met	Leu 200	Leu	Gly	His
	Ser	Asp 205	Ser	Phe	Ser	Asp	Asp 210	Lys	Val	Met	Lys	Val 215	Thr	Val	Ala	Phe
25	Asn 220	His	Phe	Gly	Pro	Asn 225	Cys	Val	Gln	Arg	Leu 230	Pro	Arg	Ala	Arg	Tyr 235
30	Gly	His	Phe	His	Val 240	Val	Asn	Asn	Asn	Tyr 245	Glu	Pro	Trp	Gly	Lys 250	Tyr
50	Ala	Ile	Gly	Gly 255	Ser	Ser	Asp	Pro	Thr 260	Ile	Ile	Ser	Glu	Gly 265	Asn	Arg
35	Phe	Leu	Ala 270	Pro	Asn	Glu	Ser	T yr 275	Lys	Lys	Glu	Val	Thr 280	Ile	Arg	Val
	Gly	Cys 285	Lys	Ser	Thr	Ser	Суs 290	Asp	Ala	Trp	Glu	Trp 295	Arg	Ser	Lys	Asp
40	Asp 300	Ala	Phe	Leu	Asn	Gly 305	Ala	Tyr	Phe	Val	Gln 310	Ser	Gly	Lys	Gly	Tyr 315
45	Asn	Gly	Gly	Glu	Ala 320	Phe	Lys	Val	Glu	Ser 325	Ala	Asn	Glu	Val	Pro 330	Thr
	Leu	Thr	Lys	His 335	Ala	Gly	Ala	Leu	Lys 340	Cys	Ile	Pro	Thr	Lys 345	Gln	Cys
50	Val	Ile														
	(2)					SEQ										
55		(1)	(<i>I</i> (I (C	A) LI B) TY C) ST	ENGTH (PE: PRANI	HARACH: 33 nuc] DEDNE DGY:	bas leic ESS:	se pa acio sino	airs 1							
60		(ii)	MOI	LECUI	E T	PE:	CDNA	A								
		(xi)	SEÇ	QUENC	CE DE	ESCRI	PTIC	ON: S	SEQ]	D NO	98:	:				
65	GGG	CTCGA	AGC 1	rgcac	TTTT	יד ידי	TTTT	CTTTT	TTT	7						
	(2)	INFO	ORMAT	NOI	FOR	SEQ	ID N	10:99) :							



5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:	
	CATAAAATGG CTTCCCCA	18
15	(2) INFORMATION FOR SEQ ID NO:100:	
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 33 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
2.5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:	
25	CGGGAATTCT AGATGTGCAA TTGTATCTTG TTA	33
30	(2) INFORMATION FOR SEQ ID NO:101:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:	
40	CGGGAATTCT AGATGTGCAA TAGTATCTTG TTG	33
	(2) INFORMATION FOR SEQ ID NO:102:	
45	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 21 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	
50	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:	
55	GGAATTCTCT AGACTGCAGG T	21
	(2) INFORMATION FOR SEQ ID NO:103:	
60	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

(ii) MOLECULE TYPE: cDNA



d	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:	
	GGAATTCTCT AGACTGCAGG TTTTTTTTTT TTTTT	35
5	(2) INFORMATION FOR SEQ ID NO:104:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:	
	GGCCTGCAGY YARCANCKKT TNSMNARNSW RCA	33
20	(2) INFORMATION FOR SEQ ID NO:105:	
25	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 17 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:	
50	CCRCTRAADA TDATCCA	17
	(2) INFORMATION FOR SEQ ID NO:106:	
35	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:	
45	GCRTCCCCRT CYTGNGGRTG	20
	(2) INFORMATION FOR SEQ ID NO:107:	
50	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:	
<i>c</i> 0	GTCCAYGGRT CRTARTTRTT	20
60	(2) INFORMATION FOR SEQ ID NO:108:	
65	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 29 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	





	(D) TOPOLOGY: linear							
	(ii) MOLECULE TYPE: cDNA							
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:							
	GCCCTGCAGT CCCCRTCYTG NGGRTGNAC	29						
10	(2) INFORMATION FOR SEQ ID NO:109:							
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 							
	(ii) MOLECULE TYPE: cDNA							
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:							
20	GCTCCACCAT GGDAGGCA	18						
	(2) INFORMATION FOR SEQ ID NO:110:							
25	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single							
30	(D) TOPOLOGY: linear							
	(ii) MOLECULE TYPE: cDNA							
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:							
35	CAYCCNCARG AYGGGGAYGC	20						
	(2) INFORMATION FOR SEQ ID NO:111:							
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 							
45	(ii) MOLECULE TYPE: cDNA							
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:							
50	CGGGAATTCC CTCARGAYGG GGAYGCNY	28						
30	(2) INFORMATION FOR SEQ ID NO:112:							
55	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 							
60	(ii) MOLECULE TYPE: cDNA							
60	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:							
	TAGGACATGA TGATACAT	18						
65								





(2)	INFORMATION FOR SEQ ID NO:113:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 18 base pairs(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:	
GAG	GATCTACA CGAGATGC	18
(2)	INFORMATION FOR SEQ ID NO:114:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:	
RAA	AWCTATTC CCTTCACT	18
(2)	INFORMATION FOR SEQ ID NO:115:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:	
TAG	GGACATAG TGATTCAT	18
(2)	INFORMATION FOR SEQ ID NO:116:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:	
CCG	GGGATCCT TACAAATAAC ACATTAT	27
(2)	INFORMATION FOR SEQ ID NO:117:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(2) TAC (2)	(A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: CDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113: GAGATCTACA CGAGATGC (2) INFORMATION FOR SEQ ID NO:114: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: CDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114: RAAWCTATTC CCTTCACT (2) INFORMATION FOR SEQ ID NO:115: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115: TAGGACATAG TGATTCAT (2) INFORMATION FOR SEQ ID NO:116: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116: CCGGGATCCT TACAAATAAC ACATTAT (2) INFORMATION FOR SEQ ID NO:117: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116: CCGGGATCCT TACAAATAAC ACATTAT





(ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:	
CCGGGATCCT TACAAATAAC ACATTAT	27
(2) INFORMATION FOR SEQ ID NO:117:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 27 base pairs(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117: CCCGAATTCA TGGCTTCCCC ATGCTTA	27
	2,
(2) INFORMATION FOR SEQ ID NO:118:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 27 base pairs(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:	
CCGGGATCCC GTTTCATAAG CAAGATT	27
(2) INFORMATION FOR SEQ ID NO:119:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 amino acids	
(B) TYPE: amino acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:</pre>	
Asp Glu Arg Thr Ala Thr Asn Ile Trp Ile Asp His Asn Ser Phe Se	er
1 5 10 15	
Asn Ser Ser Asp Asp	
20	
(2) INFORMATION FOR SEQ ID NO:120:	•
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 24 amino acids	
(B) TYPE: amino acid(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: peptide	
(v) FRAGMENT TYPE: internal	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:	

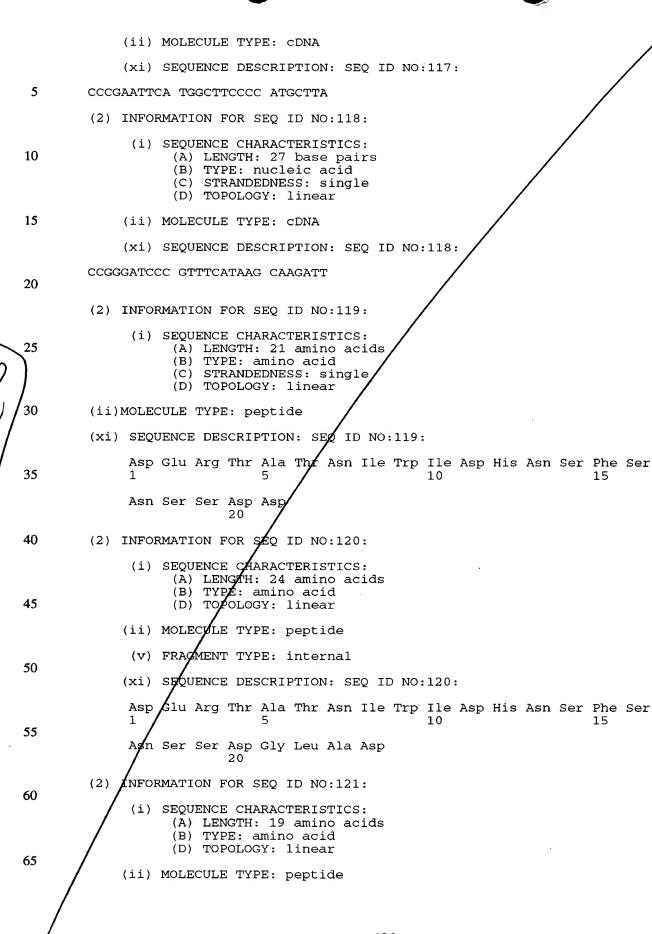
- (2) INFORMATION FOR SEQ ID NO:121:
 - (i) SEQUENCE CHARACTERISTICS:

Asn Ser Ser Asp Gly Leu Ala Asp 20

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

Asp Glu Arg Thr Ala Thr Asn Ile Trp Ile Asp His Asn Ser Phe Ser

27





4	_
•	

		(V)) FRAGMENT TYPE: internal	
5		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:121:	
3		Asp 1	o Glu Lys Ser Met Lys Ala Thr Val Ala Phe Asn Gln Phe Gly Pr 5 10 15	ro
10		Asn	n Asp Glu	
	(2)	INFO	DRMATION FOR SEQ ID NO:122:	
15		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	
20		(ii)	MOLECULE TYPE: peptide	
20		(v)	FRAGMENT TYPE: internal	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:122:	
25		Asp 1	Glu Lys Ser Met Lys Val Thr Ala Ala Phe Asn Gln Phe Gly Pi 5 10 15	ro
		Asn	n Asp Glu	
30	(2)	INFOR	DRMATION FOR SEQ ID NO:123:	
35		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	
		(ii)	MOLECULE TYPE: peptide	
40		(v)	FRAGMENT TYPE: internal	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:123:	
45		Asp 1	o Glu Glu Lys Ser Met Lys Ala Thr Val Ala Phe Asn Glu Phe Gl 5 10 15	ly
		Pro	o Asn Asp Glu Glu 20	
50	(2)	INFOR	DRMATION FOR SEQ ID NO:124:	C
55		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	
		(ii)	MOLECULE TYPE: peptide	
50		(v)	FRAGMENT TYPE: internal	
- -		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:124:	
		Asp 1	o Glu Glu Lys Ser Met Lys Val Thr Val Ala Ala Asn Gln Phe Gl 5 10 15	Ly





Pro Asn Asp Glu Glu 20

5	(2) II	IFORMA	TION I	FOR S	EQ I	D NO	:125	· :								
10			(EQUENCE (A) LEN (B) TYI (D) TOI	NGTH: PE: a	21 mino	amino acio	o ac d									
		(:	.i) MC	LECUL	TYP	E: p	eptio	đe									
15			(v) FF	RAGMENT	TYP	E: i	nter	nal									
		()	ki) SE	EQUENCI	E DES	CRIP	TION	: SE	Q II	ON C	:125	:					
20		1		u Glu	Lys	Ser 5	Met 1	Lys	Val	Thr	Val 10	Ala	Phe	Asn	Gln	Ala 15	Gly
20		I	ro As	sn Asp	Glu 20	Glu											
25	(2) II	IFORM?	TION E	FOR S	EQ I	D NO	:126	:								
		1	(QUENCE A) LEN B) TYE D) TOE	NGTH: PE: a	19 mino	amino acio	o ac d									
30		(i	i) MC	LECULE	TYP	E: p	eptio	de									
			v) FF	AGMENT	TYP	E: i	nteri	nal									
35		(3	i) SE	QUENCE	E DES	CRIP	TION	: SE	Q II	ONO:	:126	:					
		<i>I</i>		u Lys		Met 5	Lys 2	Ala	Thr	Ala	Ala 10	Phe	Asn	Gln	Phe	Gly 15	Pro
40		I	sn As	p Glu													
4.5	(2	11 (IFORMA	TION F	FOR S	EQ I	D NO	:127	:								
45		((QUENCE A) LEN B) TYE D) TOE	GTH:	21 mino	amino acio	o ac d									
50		(i	·	LECULE													
				AGMENT		_	_										
55				QUENCE					O II	NO:	:127	:					
			sp Gl	u Glu	Lys								Phe	Asn	Gln	Phe 15	Gly
60	÷	F	ro As	n Asp	Glu 20	Glu											
	(2	/I (FORMA	TION F	OR S	EQ I	D NO:	:128	:								
65		(QUENCE A) LEN													





(B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 5 (v) FRAGMENT TYPE: internal (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128: 10 Asp Asp Ala Tyr Ser Asp Asp Lys Ser Met Lys Val Thr Val Ala Phe Asn Gln Phe Gly Asp Glu 2.0 15 (2) INFORMATION FOR SEQ ID NO:129: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 amino acids 20 (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 25 (v) FRAGMENT TYPE: internal (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129: 30 Asp Lys Glu Pro Arg Ala Arg Tyr Gly Leu Val His Val Ala Asn Asn Asn Tyr Asp Pro Trp Thr Ile Glu Glu 35 (2) INFORMATION FOR SEQ ID NO:130: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 amino acids 40 (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 45 (v) FRAGMENT TYPE: internal (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130: Asp Glu Asn Gly Ala Tyr Phe Val Ser Ser Gly Lys Tyr Glu Gly Gly 50 Asn Ile Tyr Thr Lys Lys Glu Ala Phe Asn Ala Glu 55 (2) INFORMATION FOR SEQ ID NO:131: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear 60 (ii) MOLECULE TYPE: peptide (v) FRAGMENT TYPE: internal 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:





	Asp Glu Glu Asn Gly Ala Tyr Phe Val Ser Ser Gly Lys Tyr Glu Gly 1 5 10 15	
5	Gly Asn Ile Tyr Thr Lys Lys Glu Ala Phe Asn Val Glu 20 25	
	2) INFORMATION FOR SEQ ID NO:132:	
10	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 28 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: peptide	
	(v) FRAGMENT TYPE: internal	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:	
	Asp Glu Glu Gly Ala Tyr Phe Val Ser Ser Gly Lys Tyr Glu Gly Gly 1 5 10 15	
25	Asn Ile Tyr Thr Lys Lys Glu Ala Phe Asn Val Glu 20 25	
	2) INFORMATION FOR SEQ ID NO:133:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1726 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
35	(ii) MOLECULE TYPE: cDNA	
40	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 421586 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:	
45		53
50	TA ATT GCT CCA ATG GCC TTT CTG GCC ATG CAA TTG ATT ATA ATG GCG eu Ile Ala Pro Met Ala Phe Leu Ala Met Gln Leu Ile Ile Met Ala 5 10 20	01
. 55	CA GCA GAA GAT CAA TCT GCC CAA ATT ATG TTG GAC AGT GTT GTC GAA 1 1 la Ala Glu Asp Gln Ser Ala Gln Ile Met Leu Asp Ser Val Val Glu 25 30 35	49
	AA TAT CTT AGA TCG AAT CGG AGT TTA AGA AAA GTT GAG CAT TCT CGT 1 ys Tyr Leu Arg Ser Asn Arg Ser Leu Arg Lys Val Glu His Ser Arg 40 45 50	97
60	AT GAT GCT ATC AAC ATC TTC AAT GTG GAA AAG TAT GGC GCA GTA GGC 2 is Asp Ala Ile Asn Ile Phe Asn Val Glu Lys Tyr Gly Ala Val Gly	45



	GAT Asp	GGA Gly 70	AAG Lys	CAT His	GAT Asp	TGC Cys	ACT Thr 75	GAG Glu	GCA Ala	TTT Phe	TCA Ser	ACA Thr 80	GCA Ala	TGG Trp	CAA Gln	GCT Ala		293
5	GCA Ala 85	TGC Cys	AAA Lys	AAC Asn	CCA Pro	TCA Ser 90	GCA Ala	ATG Met	TTG Leu	CTT Leu	GTG Val 95	CCA Pro	GGC Gly	AGC Ser	AAG Lys	AAA Lys 100		341
10	TTT Phe	GTT Val	GTA Val	AAC Asn	AAT Asn 105	CTG Leu	TTC Phe	TTC Phe	AAT Asn	GGG Gly 110	CCA Pro	TGT Cys	CAA Gln	CCT Pro	CAC His 115	TTT Phe		389
15		TTT Phe																437
20	TGG Trp	AAG Lys	AAT Asn 135	AAT Asn	AGA Arg	ATA Ile	TGG Trp	TTG Leu 140	CAG Gln	TTT Phe	GCT Ala	AAA Lys	CTT Leu 145	ACA Thr	GGT Gly	TTT Phe		485
		CTA Leu 150																533
25		GGC Gly																581
30	GAT Asp	AGA Arg	CCA Pro	ACA Thr	GCC Ala 185	ATT Ile	AAA Lys	TTC Phe	GAT Asp	TTT Phe 190	TCC Ser	ACG Thr	GGT Gly	CTG Leu	ATA Ile 195	ATC Ile		629
35		GGA Gly																677
40	AAT Asn	TGT Cys	GAG Glu 215	GGA Gly	GTA Val	AAA Lys	ATC Ile	ATC Ile 220	GGC Gly	ATT Ile	AGT Ser	ATT Ile	ACG Thr 225	GCA Ala	CCG Pro	AGA Arg		725
4 0		AGT Ser 230																773
45		TTA Leu																821
50	GGC Gly	ACA Thr	GGG Gly	TCT Ser	TCT Ser 265	AAT Asn	ATT Ile	GTG Val	ATT Ile	GAG Glu 270	GAT Asp	CTG Leu	ATT Ile	TGC Cys	GGT Gly 275	CCA Pro		869
55		CAT His																917
60		GTT Val																965
60	AAT Asn	GGA Gly 310	TTA Leu	AGA Arg	ATC Ile	AAA Lys	ACA Thr 315	TGG Trp	CAG Gln	GGT Gly	GGT Gly	TCA Ser 320	GGC Gly	ATG Met	GCA Ala	AGC Ser	1	1013

025.5US.APP

	N	
U		
	*	

		ATA Ile															1061
5	TTA Leu	ATA Ile	AAT Asn	CAA Gln	TTC Phe 345	TAC Tyr	TGC Cys	ACT Thr	TCA Ser	GCT Ala 350	TCT Ser	GCT Ala	TGC Cys	CAA Gln	AAC Asn 355	CAG Gln	1109
10		TCT Ser															1157
15	ACA Thr	TCA Ser	GCA Ala 375	ACA Thr	GCA Ala	GCA Ala	GCA Ala	ATT Ile 380	CAA Gln	CTT Leu	AAG Lys	TGC Cys	AGT Ser 385	GAC Asp	AGT Ser	ATG Met	1205
20	CCC Pro	TGC Cys 390	AAA Lys	GAT Asp	ATA Ile	AAG Lys	CTA Leu 395	AGT Ser	GAT Asp	ATA Ile	TCT Ser	TTG Leu 400	AAG Lys	CTT Leu	ACC Thr	TCA Ser	1253
20		AAA Lys															1301
25	GGA Gly	CAC His	GTC Val	ATC Ile	CCT Pro 425	GCA Ala	TGC Cys	AAG Lys	AAT Asn	TTA Leu 430	AGT Ser	CCA Pro	AGT Ser	GCT Ala	AAG Lys 435	CGA Arg	1349
30	AAA Lys	GAA Glu	TCT Ser	AAA Lys 440	TCC Ser	CAT His	AAA Lys	CAC His	CCA Pro 445	AAA Lys	ACT Thr	GTA Val	ATG Met	GTT Val 450	GAA Glu	AAT Asn	1397
35	ATG Met	CGA Arg	GCA Ala 455	TAT Tyr	GAC Asp	AAG Lys	GGT Gly	AAC Asn 460	AGA Arg	ACA Thr	CGC Arg	ATA Ile	TTG Leu 465	TTG Leu	GGG Gly	TCG Ser	1445
40		CCT Pro 470															1493
+0		AAG Lys															1541
45		AGG Arg													TAAT	GAGATA	1593
50	CATT	rgaa <i>i</i>	ACT C	TATO	GTGCT	'A GT	GAAT	TATTO	TTC	TGGT	ACA	RTA	TAGA	AC I	GATA	TTGAA	1653
J 0	AATA	TAAL	CAT	CAATO	TTTC	T AA	AGGCZ	ATTTZ	TAP	ATAGA	ATTA	TATT	TAATO	GT 1	CAGC	CTGGT	1713
	GCAZ	AAAA	AAA A	AA													1726
55	(2)	INFO	RMAT	NOI	FOR	SEQ	ID N	10:13	4:								
		((i) S	(A)	ENCE LEN	IGTH:	514	l ami	no a		;						
50				(B) (D)	TYF TOF	PE: a											

(ii) MOLECULE TYPE: protein





(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

5	Met 1	Ala	Met	Lys	Leu 5	Ile	Ala	Pro	Met	Ala 10	Phe	Leu	Ala	Met	Gln 15	Leu
3	Ile	Ile	Met	Ala 20	Ala	Ala	Glu	Asp	Gln 25	Ser	Ala	Gln	Ile	Met 30	Leu	Asp
10	Ser	Val	Val 35	Glu	Lys	Tyr	Leu	Arg 40	Ser	Asn	Arg	Ser	Leu 45	Arg	Lys	Val
·	Glu	His 50	Ser	Arg	His	Asp	Ala 55	Ile	Asn	Ile	Phe	Asn 60	Val	Glu	Lys	Tyr
15	Gly 65	Ala	Val	Gly	Asp	Gly 70	Lys	His	Asp	Cys	Thr 75	Glu	Ala	Phe	Ser	Thr 80
20	Ala	Trp	Gln	Ala	Ala 85	Cys	Lys	Asn	Pro	Ser 90	Ala	Met	Leu	Leu	Val 95	Pro
20	Gly	Ser	Lys	Lys 100	Phe	Val	Val	Asn	Asn 105	Leu	Phe	Phe	Asn	Gly 110	Pro	Cys
25	Gln	Pro	His 115	Phe	Thr	Phe	Lys	Val 120	Asp	Gly	Ile	Ile	Ala 125	Ala	Tyr	Gln
	Asn	Pro 130	Ala	Ser	Trp	Lys	Asn 135	Asn	Arg	Ile	Trp	Leu 140	Gln	Phe	Ala	Lys
30	Leu 145	Thr	Gly	Phe	Thr	Leu 150	Met	Gly	Lys	Gly	Val 155	Ile	Asp	Gly	Gln	Gly 160
35	Lys	Gln	Trp	Trp	Ala 165	Gly	Gln	Cys	Lys	Trp 170	Val	Asn	Gly	Arg	Glu 175	Ile
	Cys	Asn	Asp	Arg 180	Asp	Arg	Pro	Thr	Ala 185	Ile	Lys	Phe	Asp	Phe 190	Ser	Thr
40	Gly	Leu	Ile 195	Ile	Gln	Gly	Leu	Lys 200	Leu	Met	Asn	Ser	Pro 205	Glu	Phe	His
	Leu	Val 210	Phe	Gly	Asn	Cys	Glu 215	Gly	Val	Lys	Ile	Ile 220	Gly	Ile	Ser	Ile
45	Thr 225	Ala	Pro	Arg	Asp	Ser 230	Pro	Asn	Thr	Asp	Gly 235	Ile	Asp	Ile	Phe	Ala 240
50	Ser	Lys	Asn		His 245		Gln	Lys		Thr 250	Ile	Gly	Thr	Gly	Asp 255	Asp
	Cys	Val	Ala	Ile 260	Gly	Thr	Gly	Ser	Ser 265	Asn	Ile	Val	Ile	Glu 270	Asp	Leu
55	Ile	Cys	Gly 275	Pro	Gly	His	Gly	Ile 280	Ser	Ile	Gly	Ser	Leu 285	Gly	Arg	Glu
	Asn	Ser 290	Arg	Ala	Glu	Val	Ser 295	Tyr	Val	His	Val	Asn 300	Gly	Ala	Lys	Phe
60	Ile 305	Asp	Thr	Gln	Asn	Gly 310	Leu	Arg	Ile	Lys	Thr 315	Trp	Gln	Gly	Gly	Ser 320
65	Gly	Met	Ala	Ser	His 325	Ile	Ile	Tyr	Glu	Asn 330	Val	Glu	Met	Ile	Asn 335	Ser





	GIU	Asn	Pro	340	Leu	11e	Asn	GIN	345	Tyr	Cys	Thr	ser	350	ser	Aľa	
5	Cys	Gln	Asn 355	Gln	Arg	Ser	Ala	Val 360	Gln	Ile	Gln	Asp	Val 365	Thr	Tyr	Lys	
	Asn	Ile 370	Arg	Gly	Thr	Ser	Ala 375	Thr	Ala	Ala	Ala	Ile 380	Gln	Leu	Lys	Cys	
10	Ser 385	Asp	Ser	Met	Pro	Cys 390	Lys	Asp	Ile	Lys	Leu 395	Ser	Asp	Ile	Ser	Leu 400	
15	Lys	Leu	Thr	Ser	Gly 405	Lys	Ile	Ala	Ser	Cys 410	Leu	Asn	Asp	Asn	Ala 415	Asn	
15	Gly	Tyr	Phe	Ser 420	Gly	His	Val	Ile	Pro 425	Ala	Cys	Lys	Asn	Leu 430	Ser	Pro	
20	Ser	Ala	Lys 435	Arg	Lys	Glu	Ser	Lys 440	Ser	His	Lys	His	Pro 445	Lys	Thr	Val	
	Met	Val 450	Glu	Asn	Met	Arg	Ala 455	Tyr	Asp	Lys	Gly	Asn 460	Arg	Thr	Arg	Ile	
25	Leu 465	Leu	Gly	Ser	Arg	Pro 470	Pro	Asn	Cys	Thr	Asn 475	Lys	Cys	His	Gly	Cys 480	
30	Ser	Pro	Cys	Lys	Ala 485	Lys	Leu	Val	Ile	Val 490	His	Arg	Ile	Met	Pro 495	Gln	
30	Glu	Tyr	Tyr	Pro 500	Gln	Arg	Trp	Ile	Cys 505	Ser	Cys	His	Gly	Lys 510	Ile	Tyr	
35	His	Pro															
	(2)	INFO	ORMAT	rion	FOR	SEQ	ID 1	10:13	35:								
40		(i)	(/ (I	A) LH 3) TY	CE CH ENGTH (PE: OPOLO	4: 45 amir	am:	ino a	CS: acids	5							
45		(ii)	MOI	ECUI	LE TY	PE:	pept	ide									
+5		(v)	FRA	AGMEN	7T T	PE:	inte	ernal	l.								
		(xi)	SEÇ	QUENC	CE DE	ESCRI	PTIC	ON: S	SEQ I	D NO	0:135	5:					
50		Arg 1	d FA	val	l Glu	u His 5	s Sei	r Arg	g His	s Asp) Alá 10	a Ile	e Ası	n Ile	e Phe	Asn 15	Va:
55		Glu	ı Lys	туі	Gly 20	/ Ala	a Val	l Gly	y Asr	Gly 25	/ Lys	s His	s Asp	Cys	Thi 30	Glu	Alá
		Phe	e Sei	Thi 35	Ala	a Trp	Glr	n Alá	a Ala 40	a Cys	s Lys	s Asr	n Pro	Ser 45	?		
60	(2)	INFO	ORMAT	NOI	FOR	SEQ	ID N	10:13	36:								
		(i)	(E	A) LE 3) TY		4: 41 amir	l ami	ino a cid	CS: acids	5					٠		
65		(ii)	MOI	ECUI	E TY	PE:	pept	ide									





		(V)	FRAC	GMEN'	r TY	PE:	inte	rnal									
5		(xi)	SEQU	JENCI	E DE	SCRI	PTIO	1: S	EQ II	ON C	:136	:					
3		Arg 1	Lys	Val	Glu	His 5	Ser	Arg	His	Asp	Ala 10	Ile	Asn	Ile	Phe	Asn 15	Val
10		Glu	Lys	Tyr	Gly 20	Ala	Val	Gly	Asp	Gly 25	Lys	His	Asp	Cys	Thr 30	Glu	Ala
		Phe	Ser	Thr 35	Ala	Trp	Gln	Lys	Asn 40	Pro							
15	(2)	INFO	RMAT	ION I	FOR S	SEQ :	ID N	0:13	7:								
20		(i)	(B)	LE1	NGTH PE: 8	: 36 amin	TERIS amin o aci	no ao id									
		(ii)	MOLE	ECULI	E TY	PE: 1	pept:	iđe									
25		(v)	FRAC	GMENT	r TYI	PE:	inte	rnal									
23		(xi)	SEQU	JENCI	E DES	SCRI	OITG	1: SI	EQ II	ON C	:137	•					
30		Ser 1	Arg	His	Asp	Ala 5	Ile	Asn	Ile	Phe	Asn 10	Val	Glu	Lys	Tyr	Gly 15	Ala
30		Val	Gly	Asp	Gly 20	Lys	His	Asp	Cys	Thr 25	Glu	Ala	Phe	Ser	Thr 30	Ala	Trp
35		Gln	Lys	Asn 35	Pro												
	(2)	INFO	RMATI	ON I	FOR S	SEQ :	ID NO	0:138	3:								
40		(i)	(Ã) (B)	LEN TYP	NGTH:	: 10 amino	reris amir aci lines	no ao id									
45		(ii)	MOLE	ECULE	TYI	PE: p	pepti	ide									
		(v)	FRAC	SMENT	TYI	PE: :	inter	nal									
50		(xi)	SEQU	J EN CE	E DES	SCRI	OITS	1: SI	EQ II	NO:	138:	:					
30		Ala 1	Ile	Asn	Ile	Phe 5	Asn	Val	Glu	Lys	Tyr 10						
55	(2)	INFOR	RMATI	ON E	FOR S	SEQ I	ID NO	139	:								
~~		(i)		LEN	IGTH:	: 143	FERIS 10 ba ∋ic a	ase p		5							
60							SS: s linea		le								
		(ii)	MOLE	CULE	TYI	PE: 0	DNA										





(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

	AGAAAAGTTG AGCATTCTCG TCATGATGCT ATCAACATCT TCAATGTGGA AAAGTATGGC	60
5	GCAGTAGGCG ATGGAAAGCA TGATTGCACT GAGGCATTTT CAACAGCATG GCAAGCTGCA	120
	TGCAAAAACC CATCAGCAAT GTTGCTTGTG CCAGGCAGCA AGAAATTTGT TGTAAACAAT	180
10	CTGTTCTTCA ATGGGCCATG TCAACCTCAC TTTACTTTTA AGGTAGATGG GATAATAGCT	240
10	GCGTACCAAA ATCCAGCGAG CTGGAAGAAT AATAGAATAT GGTTGCAGTT TGCTAAACTT	300
	ACAGGTTTTA CTCTAATGGG TAAAGGTGTA ATTGATGGGC AAGGAAAACA ATGGTGGGCT	360
15	GGCCAATGTA AATGGGTCAA TGGACGAGAA ATTTGCAACG ATCGTGATAG ACCAACAGCC	420
	ATTAAATTCG ATTTTTCCAC GGGTCTGATA ATCCAAGGAC TGAAACTAAT GAACAGTCCC	480
20	GAATTTCATT TAGTTTTTGG GAATTGTGAG GGAGTAAAAA TCATCGGCAT TAGTATTACG	540
20	GCACCGAGAG ACAGTCCTAA CACTGATGGA ATTGATATCT TTGCATCTAA AAACTTTCAC	600
	TTACAAAAGA ACACGATAGG AACAGGGGAT GACTGCGTCG CTATAGGCAC AGGGTCTTCT	660
25	AATATTGTGA TTGAGGATCT GATTTGCGGT CCAGGCCATG GAATAAGTAT AGGAAGTCTT	720
	GGGAGGGAAA ACTCTAGAGC AGAGGTTTCA TACGTGCACG TAAATGGGGC TAAATTCATA	780
30	GACACAAA ATGGATTAAG AATCAAAACA TGGCAGGGTG GTTCAGGCAT GGCAAGCCAT	840
30	ATAATTTATG AGAATGTTGA AATGATAAAT TCGGAGAACC CCATATTAAT AAATCAATTC	900
	TACTGCACTT CAGCTTCTGC TTGCCAAAAC CAGAGGTCTG CGGTTCAAAT CCAAGATGTG	960
35	ACATACAAGA ACATACGTGG GACATCAGCA ACAGCAGCAG CAATTCAACT TAAGTGCAGT	1020
	GACAGTATGC CCTGCAAAGA TATAAAGCTA AGTGATATAT CTTTGAAGCT TACCTCAGGG	1080
40	AAAATTGCTT CCTGCCTTAA TGATAATGCA AATGGATATT TCAGTGGACA CGTCATCCCT	1140
40	GCATGCAAGA ATTTAAGTCC AAGTGCTAAG CGAAAAGAAT CTAAATCCCA TAAACACCCA	1200
	AAAACTGTAA TGGTTGAAAA TATGCGAGCA TATGACAAGG GTAACAGAAC ACGCATATTG	1260
45	TTGGGGTCGA GGCCTCCGAA TTGTACAAAC AAATGTCATG GTTGCAGTCC ATGTAAGGCC	1320
	AAGTTAGTTA TTGTTCATCG TATTATGCCG CAGGAGTATT ATCCTCAGAG GTGGATATGC	1380
50	AGCTGTCATG GCAAAATCTA CCATCCATAA	1410

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1395 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 60 (ii) MOLECULE TYPE: cDNA

60





(xl)	SEQUENCE	DESCRIPTION:	SEQ	ID	NO:140:
------	----------	--------------	-----	----	---------

	TCTCGTCATG	ATGCTATCAA	CATCTTCAAT	GTGGAAAAGT	ATGGCGCAGT	AGGCGATGGA	60
5	AAGCATGATT	GCACTGAGGC	ATTTTCAACA	GCATGGCAAG	CTGCATGCAA	AAACCCATCA	120
	GCAATGTTGC	TTGTGCCAGG	CAGCAAGAAA	TTTGTTGTAA	ACAATCTGTT	CTTCAATGGG	180
10	CCATGTCAAC	CTCACTTTAC	TTTTAAGGTA	GATGGGATAA	TAGCTGCGTA	ССААААТССА	240
10	GCGAGCTGGA	AGAATAATAG	AATATGGTTG	CAGTTTGCTA	AACTTACAGG	TTTTACTCTA	300
	ATGGGTAAAG	GTGTAATTGA	TGGGCAAGGA	AAACAATGGT	GGGCTGGCCA	ATGTAAATGG	360
15	GTCAATGGAC	GAGAAATTTG	CAACGATCGT	GATAGACCAA	CAGCCATTAA	ATTCGATTTT	420
	TCCACGGGTC	TGATAATCCA	AGGACTGAAA	CTAATGAACA	GTCCCGAATT	TCATTTAGTT	480
	TTTGGGAATT	GTGAGGGAGT	AAAAATCATC	GGCATTAGTA	TTACGGCACC	GAGAGACAGT	540
20	CCTAACACTG	ATGGAATTGA	TATCTTTGCA	ТСТАААААСТ	TTCACTTACA	AAAGAACACG	600
	ATAGGAACAG	GGGATGACTG	CGTCGCTATA	GGCACAGGGT	СТТСТААТАТ	TGTGATTGAG	660
25	GATCTGATTT	GCGGTCCAGG	CCATGGAATA	AGTATAGGAA	GTCTTGGGAG	GGAAAACTCT	720
		TTTCATACGT					780
	TTAAGAATCA	AAACATGGCA	GGGTGGTTCA	GGCATGGCAA	GCCATATAAT	TTATGAGAAT	840
30	GTTGAAATGA	TAAATTCGGA	GAACCCCATA	ТТААТАААТС	AATTCTACTG	CACTTCAGCT	900
		AAAACCAGAG					960
35		CAGCAACAGC					1020
		AGCTAAGTGA					1020
		ATGCAAATGG					1140
40		CTAAGCGAAA					1200
							1260
45		GAGCATATGA					
45		CAAACAAATG					1320
			GTATTATCCT	CAGAGGTGGA	TATGCAGCTG	TCATGGCAAA	
50	ATCTACCATC			,			1395
	(A) TATEODAC	1 TANK TANK	30 TO 310 1 4	•			

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1479 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:
- GAAGATCAAT CTGCCCAAAT TATGTTGGAC AGTGTTGTCG AAAAATATCT TAGATCGAAT

55



4	قنسا	
	М	

	CGGAGTTTAA GAAAAGTTGA GCATTCTCGT CATGATGCTA TCAACATCTT CAATGTGGAA	120
	AAGTATGGCG CAGTAGGCGA TGGAAAGCAT GATTGCACTG AGGCATTTTC AACAGCATGG	180
5	CAAGCTGCAT GCAAAAACCC ATCAGCAATG TTGCTTGTGC CAGGCAGCAA GAAATTTGTT	240
	GTAAACAATC TGTTCTTCAA TGGGCCATGT CAACCTCACT TTACTTTTAA GGTAGATGGG	300
10	ATAATAGCTG CGTACCAAAA TCCAGCGAGC TGGAAGAATA ATAGAATATG GTTGCAGTTT	360
10	GCTAAACTTA CAGGTTTTAC TCTAATGGGT AAAGGTGTAA TTGATGGGCA AGGAAAACAA	420
	TGGTGGGCTG GCCAATGTAA ATGGGTCAAT GGACGAGAAA TTTGCAACGA TCGTGATAGA	480
15	CCAACAGCCA TTAAATTCGA TTTTTCCACG GGTCTGATAA TCCAAGGACT GAAACTAATG	540
	AACAGTCCCG AATTTCATTT AGTTTTTGGG AATTGTGAGG GAGTAAAAAT CATCGGCATT	600
20	AGTATTACGG CACCGAGAGA CAGTCCTAAC ACTGATGGAA TTGATATCTT TGCATCTAAA	660
20	AACTTTCACT TACAAAAGAA CACGATAGGA ACAGGGGATG ACTGCGTCGC TATAGGCACA	720
	GGGTCTTCTA ATATTGTGAT TGAGGATCTG ATTTGCGGTC CAGGCCATGG AATAAGTATA	780
25	GGAAGTCTTG GGAGGGAAAA CTCTAGAGCA GAGGTTTCAT ACGTGCACGT AAATGGGGCT	840
	AAATTCATAG ACACAAAAA TGGATTAAGA ATCAAAACAT GGCAGGGTGG TTCAGGCATG	900
30	GCAAGCCATA TAATTTATGA GAATGTTGAA ATGATAAATT CGGAGAACCC CATATTAATA	960
30	AATCAATTCT ACTGCACTTC AGCTTCTGCT TGCCAAAACC AGAGGTCTGC GGTTCAAATC	1020
	CAAGATGTGA CATACAAGAA CATACGTGGG ACATCAGCAA CAGCAGCAGC AATTCAACTT	1080
35	AAGTGCAGTG ACAGTATGCC CTGCAAAGAT ATAAAGCTAA GTGATATATC TTTGAAGCTT	1140
	ACCTCAGGGA AAATTGCTTC CTGCCTTAAT GATAATGCAA ATGGATATTT CAGTGGACAC	1200
40	GTCATCCCTG CATGCAAGAA TTTAAGTCCA AGTGCTAAGC GAAAAGAATC TAAATCCCAT	1260
40	AAACACCCAA AAACTGTAAT GGTTGAAAAT ATGCGAGCAT ATGACAAGGG TAACAGAACA	1320
	CGCATATTGT TGGGGTCGAG GCCTCCGAAT TGTACAAACA AATGTCATGG TTGCAGTCCA	1380
45	TGTAAGGCCA AGTTAGTTAT TGTTCATCGT ATTATGCCGC AGGAGTATTA TCCTCAGAGG	1440
	TGGATATGCA GCTGTCATGG CAAAATCTAC CATCCATAA	1479
50	(2) INFORMATION FOR SEQ ID NO:142:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
55	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
60	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:	
	RTAYTTYTCN ACRTTRAA	18
	(2) INFORMATION FOR SEQ ID NO:143:	
65	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 6 amino acids	





	(B) TYPE: amino acid (D) TOPOLOGY: linear	
_	(ii) MOLECULE TYPE: peptide	
5	(v) FRAGMENT TYPE: internal	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:	
	Phe Asn Val Glu Lys Tyr 1 5	
15	(2) INFORMATION FOR SEQ ID NO:144:	
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 27 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:	
	CCTGCAGTAY TTYTCNACRT TRAANAT	27
30	(2) INFORMATION FOR SEQ ID NO:145:	
30	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 7 base pairs(B) TYPE: nucleic acid	
35	<pre>(C) STRANDEDNESS: single (D) TOPOLOGY: linear</pre>	
	(ii) MOLECULE TYPE: cDNA	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:	
	CCTGCAG	7
	(2) INFORMATION FOR SEQ ID NO:146:	
45	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 7 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	·
50	(ii) MOLECULE TYPE: peptide	
	(v) FRAGMENT TYPE: internal	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:	
	Ile Phe Asn Val Glu Lys Tyr 1 5	
60	(2) INFORMATION FOR SEQ ID NO:147:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 27 base pairs(B) TYPE: nucleic acid	
65	<pre>(C) STRANDEDNESS: single (D) TOPOLOGY: linear</pre>	



		•
YPE:	CDNA	

	(II) MOLECULE TYPE: CDNA	٠
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:	
5	CCTGCAGTAY TTYTCNACRT TRAADAT	27
	(2) INFORMATION FOR SEQ ID NO:148:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
15	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:	
20	GCNATHAAYA THTTYAA	17
20	(2) INFORMATION FOR SEQ ID NO:149:	
25	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 6 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: peptide	
30	(v) FRAGMENT TYPE: internal	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:	
35	Ala Ile Asn Ile Phe Asn 1 5	
	(2) INFORMATION FOR SEQ ID NO:150:	
40	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 28 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:	
50	GGAATTCCGC NATHAAYATH TTYAAYGT	28
50	(2) INFORMATION FOR SEQ ID NO:151:	
55	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 8 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
60	(ii) MOLECULE TYPE: cDNA	
5 0	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:	
	GGAATTCC	8
65	(2) INFORMATION FOR SEQ ID NO:152:	





	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 7 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: peptide	
	(v) FRAGMENT TYPE: internal	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:	
	Ala Ile Asn Ile Phe Asn Val	
15	(2) INFORMATION FOR SEQ ID NO:153:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:	
	GCYTCNGTRC ARTCRTGYTT	20
30	(2) INFORMATION FOR SEQ ID NO:154:	
30	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 7 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: peptide	
	(v) FRAGMENT TYPE: internal	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:	
	Lys His Asp Cys Thr Glu Ala 1 5	
45	(2) INFORMATION FOR SEQ ID NO:155:	
50	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 28 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:	
	GGCTGCAGGT RCARTCRTGY TTNCCRTC	28
60	(2) INFORMATION FOR SEQ ID NO:156:	
60	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 8 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	
65	(D) TOPOLOGY: linear	





	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:	
5	GGCTGCAG	8
	(2) INFORMATION FOR SEQ ID NO:157:	
10	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 7 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: peptide	
15	(v) FRAGMENT TYPE: internal	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:	
20	Asp Gly Lys His Asp Cys Thr 1 5	
	(2) INFORMATION FOR SEQ ID NO:158:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
30	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:	
35	ATGTTGGACA GTGTTGTCGA A	21
	(2) INFORMATION FOR SEQ ID NO:159:	21
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:	
50	GGGAATTCAG AAAAGTTGAG CATTCTCGT	29
30	(2) INFORMATION FOR SEQ ID NO:160:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 8 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
60	(ii) MOLECULE TYPE: cDNA	
60	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:	
	GGGAATTC	8
65	(2) INFORMATION FOR SEQ ID NO:161:	



5	(1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161: GTTCTTCAAT GGGCCATGT	19
	(2) INFORMATION FOR SEQ ID NO:162:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
20	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:	
25	GTGTTAGGAC TGTCTCTCGG	20
	(2) INFORMATION FOR SEQ ID NO:163:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
35	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:	
	TGTCCAGGCC ATGGAATAAG	20
40	(2) INFORMATION FOR SEQ ID NO:164:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: cDNA	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:	
	GCCTTACATG GACTGCAACC	20
55	(2) INFORMATION FOR SEQ ID NO:165:	
60	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	



	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:	
	TCCACGGGTC TGATAATCCA	20
5	(2) INFORMATION FOR SEQ ID NO:166:	
10	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:	
	AGGCAGGAAG CAATTTTCCC	20
20	(2) INFORMATION FOR SEQ ID NO:167:	
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:	
	TACTGCACTT CAGCTTCTGC	20
35	(2) INFORMATION FOR SEQ ID NO:168:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:	
	GGGGGTCTCC GAATTTATCA	20
50	(2) INFORMATION FOR SEQ ID NO:169:	
55	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:	
60	GGATATTTCA GTGGACACGT	20
	(2) INFORMATION FOR SEQ ID NO:170:	== +
65	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs	



	(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:	
10	TATTAGAAGA CCCTGCGCCT	20
, , , , , , , , , , , , , , , , , , ,	(2) INFORMATION FOR SEQ ID NO:171:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:	
25	CCATGTAAGG CCAAGTTAGT	20
	(2) INFORMATION FOR SEQ ID NO:172:	
30	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:	
40	ACACCTTTAC CCATTAGAGT	20
40	(2) INFORMATION FOR SEQ ID NO:173:	
45	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: cDNA	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:	
	CTGTCCAACA TAATTTGGGC	20
55	(2) INFORMATION FOR SEQ ID NO:174:	
60	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: cDNA



	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:	
	CATGGCAGGG TGGTTCAGGC	20
5	(2) INFORMATION FOR SEQ ID NO:175:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:	
	TAGCCCCATT TACGTGCACG	20
20	(2) INFORMATION FOR SEQ ID NO:176:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:	
	TTGGGGTCGA GGCCTCCGAA	20
35	(2) INFORMATION FOR SEQ ID NO:177:	
40	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 9 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:	
43	TAAAAUGGC	9
	(2) INFORMATION FOR SEQ ID NO:178:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 9 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
55	(ii) MOLECULE TYPE: cDNA	
60	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178: AACAAUGGC	9
	,	3
	(2) INFORMATION FOR SEQ ID NO:179:	
65	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 27 base pairs(B) TYPE: nucleic acid	



(C) STRANDEDNESS: single

	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:	
10	GCCGAATTCA TGGCCATGAA ATTAATT	27
	(2) INFORMATION FOR SEQ ID NO:180:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 9 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
20	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:	
	GCCGAATTC	9
25	(2) INFORMATION FOR SEQ ID NO:181:	
30	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 27 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	,
35	(ii) MOLECULE TYPE: cDNA	
33	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:	
	CGGGGATCCT CATTATGGAT GGTAGAT	. 27
40	(2) INFORMATION FOR SEQ ID NO:182:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 9 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:	
	CGGGGATCC	9
55	(2) INFORMATION FOR SEQ ID NO:183:	
55	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 13 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
60	(ii) MOLECULE TYPE: peptide	
	(v) FRAGMENT TYPE: internal	
65		





		(X1) SEQUENCE DESCRIPTION: SEQ ID NO:183:	
5		Phe Thr Phe Lys Val Asp Gly Ile Ile Ala Ala Tyr Gln 1 5	10
3	(2)	INFORMATION FOR SEQ ID NO:184:	
10		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 14 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
		(ii) MOLECULE TYPE: peptide	
15		(v) FRAGMENT TYPE: internal	
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:	
20		Asn Gly Tyr Phe Ser Gly His Val Ile Pro Ala Cys Lys Asn 1	10
	(2)	INFORMATION FOR SEQ ID NO:185:	
25		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 13 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
30		(ii) MOLECULE TYPE: peptide	
30		(v) FRAGMENT TYPE: internal	
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:	
35		Phe Thr Phe Lys Val Asp Gly Ile Ile Ala Ala Tyr Gln 1 5 10	
	(2)	INFORMATION FOR SEQ ID NO:186:	
40		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 14 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
45		(ii) MOLECULE TYPE: peptide	
		(v) FRAGMENT TYPE: internal	
50		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:	
50		Asn Gly Tyr Phe Ser Gly His Val Ile Pro Ala Cys Lys Asn 1 10	
55	(2)	INFORMATION FOR SEQ ID NO:187:	
<i>აა</i>		(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 128 amino acids	
60		(B) TYPE: amino acid (D) TOPOLOGY: linear	
		(ii) MOLECULE TYPE: peptide	
65		(v) FRAGMENT TYPE: internal	





		(X1)	SEQU	JENC	E DES	SCRII	PTIO	V: SI	EQ II	O NO	:187	:					
5		Met 1	Gly	His	His	His 5	His	His	His	Glu	Phe 10	Arg	Lys	Val	Glu	His 15	Ser
3		Arg	His	Asp	Ala 20	Ile	Asn	Ile	Phe	Asn 25	Val	Glu	Lys	Tyr	Gly 30	Ala	Val
10		Gly	Asp	Gly 35	Lys	His	Asp	Cys	Thr 40	Glu	Ala	Phe	Ser	Thr 45	Ala	Trp	Glr
		Ala	Ala 50	Cys	Lys	Asn	Pro	Ser 55	Ala	Met	Leu	Leu	Val 60	Pro	Gly	Ser	Lys
15		Lys 65	Phe	Val	Val	Asn	Asn 70	Leu	Phe	Phe	Asn	Gly 75	Pro	Суѕ	Gln	Pro	His 80
20		Phe	Thr	Phe	Lys	Val 85	Asp	Gly	Ile	Ile	Ala 90	Ala	Tyr	Gln	Asn	Pro 95	Ala
		Ser	Trp	Lys	Asn 100	Asn	Arg	Ile	Trp	Leu 105	Gln	Phe	Ala	Lys	Leu 110	Thr	Gly
25		Phe	Thr	Leu 115	Met	Gly	Lys	Gly	Val 120	Ile	Asp	Gly	Gln	Gly 125	Lys	Gln	Trp
	(2)	INFO	RMAT:	I NOI	FOR S	SEQ I	ID NO	188	3:								
30		(i)	(Ã)	LEI TYI	E CHANGTH PE: &	: 127	7 ami	ino a id		5							
		(ii)	MOLI	ECULI	E TYI	PE: r	pept	ide									
35		(v)	FRAG	GMENT	r TYI	PE: :	inte	rnal									
		(xi)	SEQU	JENCI	E DES	SCRI	OIT9	V: SI	EQ II	ON C	:188	:					
40		Met 1	Gly	His	His	His 5	His	His	His	Glu	Phe 10	Trp	Ala	Gly	Gln	Cys 15	Lys
45		Trp	Val	Asn	Gly 20	Arg	Glu	Ile	Cys	Asn 25	Asp	Arg	Asp	Arg	Pro 30	Thr	Ala
		Ile	Lys	Phe 35	Asp	Phe	Ser	Thr	Gly 40	Leu	Ile	Ile	Gln	Gly 45	Leu	Lys	Leu
50		Met	Asn 50	Ser	Pro	Glu	Phe	His 55	Leu	Val	Phe	Gly	Asn 60	Cys	Glu	Gly	Val
		Lys 65	Ile	Ile	Gly	Ile	Ser 70	Ile	Thr	Ala	Pro	Arg 75	Asp	Ser	Pro	Asn	Thr 80
55		Asp	Gly	Ile	Asp	Ile 85	Phe	Ala	Ser	Lys	Asn 90	Phe	His	Leu	Gln	Lys 95	Asn
60		Thr	Ile	Gly	Thr 100	Gly	Asp	Asp	Cys	Val 105	Ala	Ile	Gly	Thr	Gly 110	Ser	Ser
55		Asn	Ile	Val 115	Ile	Glu	Asp	Leu	Ile 120	Cys	Gly	Pro	Gly	His 125	Gly	Ile	
65	(2)	INFO	RMAT	гои і	FOR S	SEQ I	ID NO	189	€:								

(i) SEQUENCE CHARACTERISTICS:





- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- 5 (ii) MOLECULE TYPE: peptide

15

20

25

30

45

55

60

- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Met Gly His His His His His Glu Phe Ser Ile Gly Ser Leu Gly 1 5 10 15

Arg Glu Asn Ser Arg Ala Glu Val Ser Tyr Val His Val Asn Gly Ala 20 25 30

Lys Phe Ile Asp Thr Gln Asn Gly Leu Arg Ile Lys Thr Trp Gln Gly 35 40 45

Gly Ser Gly Met Ala Ser His Ile Ile Tyr Glu Asn Val Glu Met Ile 50 60

Asn Ser Glu Asn Pro Ile Leu Ile Asn Gln Phe Tyr Cys Thr Ser Ala 65 70 75 80

Ser Ala Cys Gln Asn Gln Arg Ser Ala Val Gln Ile Gln Asp Val Thr 85 90 95

Tyr Lys Asn Ile Arg Gly Thr Ser Ala Thr Ala Ala Ile Gln Leu 100 105 110

Lys Cys Ser Asp Ser Met Pro Cys Lys Asp Ile Lys Leu Ser Asp 115 120 125

- 35 (2) INFORMATION FOR SEQ ID NO:190:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 amino acids
 - (B) TYPE: amino acid
- 40 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (v) FRAGMENT TYPE: internal
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Met Gly His His His His His Glu Phe Ile Ser Leu Lys Leu Thr 50 1 5 10 15

Ser Gly Lys Ile Ala Ser Cys Leu Asn Asp Asn Ala Asn Gly Tyr Phe 20 25 30

Ser Gly His Val Ile Pro Ala Cys Lys Asn Leu Ser Pro Ser Ala Lys 35 40 45

Arg Lys Glu Ser Lys Ser His Lys His Pro Lys Thr Val Met Val Glu 50 60

Asn Met Arg Ala Tyr Asp Lys Gly Asn Arg Thr Arg Ile Leu Leu Gly 65 70 75 80





			ser	Arg	Pro	Pro	Asn 85	Cys	Thr	Asn	Lys	Cys 90	His	Gly	Cys	Ser	Pro 95	Cys
5			Lys	Ala	Lys	Leu 100	Val	Ile	Val	His	Arg 105	Ile	Met	Pro	Gln	Glu 110	Tyr	Tyr
			Pro	Gln	Arg 115	Trp	Ile	Cys	Ser	Cys 120	His	Gly	Lys	Ile	Tyr 125	His	Pro	
10	(2	2)	INFOR	TAMS	ION I	FOR :	SEQ :	ID N	0:19	1:								
15			(i)	(A) (B)	LEN TYI	NGTH PE: 6	ARAC' : 24 amin	ami o ac	no a id									
			(ii)	MOLE	ECULI	E TY	PE:]	pept	ide									
20			(v)	FRAC	SMENT	r TY	PE:	inte:	rnal									
			(xi)	SEQU	JENCI	E DE	SCRI	PTIO	N: S	EQ II	ои с	:191	:					
25			Gly 1	Lys	Gly	Val	Ile 5	Asp	Gly	Gln	Gly	Lys 10	Gln	Trp	Trp	Ala	Gly 15	Gln
30			Cys	Lys	Trp	Val 20	Asn	Gly	Arg	Glu								
30	(2	2)	INFOR	(TAMS	ON E	FOR S	SEQ :	ID N	0:192	2:								
35			(i)	(B)	LEN TYE	NGTH PE: 8	ARAC' : 24 amin	amin ac:	no ao id									
			(ii)	MOLE	CULE	TYI	PE: I	pept	ide									
40			(v)	FRAC	MENT	г түі	PE:	inte	rnal									
			(xi)	SEQU	JENCE	E DES	SCRII	PTIO	N: SI	EQ II	ои с	:192	:					
45			Asp 1	Ser	Met	Pro	Cys 5	Lys	Asp	Ile	Lys	Leu 10	Ser	Asp	Ile	Ser	Leu 15	Lys
50			Leu	Thr	Ser	Gly 20	Lys	Ile	Ala	Ser								
50	(2	2)	INFOF	TAM!	ON F	FOR S	SEQ I	ID NO	193	3:								
55			(i)	(B)	LEN TYF	NGTH:	ARACT : 24 amino GY: 1	amin ac:	no ao id									
			(ii)	MOLE	CULE	TYI	PE: p	pept:	ide									
60			(v)	FRAC	MENT	TYI	PE: 3	inte	rnal									
65			(xi)	SEQU	JENCE	E DES	SCRII	OITS	N: SI	EQ II	ONO	:193	:					





	Ile Glu Asp Leu Ile Cys Gly Pro Gly His Gly Ile Ser Ile Gly Ser 1 5 10 15	
5	Leu Gly Arg Glu Asn Ser Arg Ala 20	
	(2) INFORMATION FOR SEQ ID NO:194:	
10	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 21 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
15	(ii)	
	MOLECULE TYPE: cDNA	
20	<pre>(ix) FEATURE: (A) NAME/KEY: modified_base (B) LOCATION: 6, 15 (D) OTHER INFORMATION: /mod_base= i</pre>	
	(xi)	
25	SEQUENCE DESCRIPTION: SEQ ID NO:194:	
	AAYCCNATHG AYWSNCGYTG G	21
	(2) INFORMATION FOR SEQ ID NO:195:	
30	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 23 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	
35	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
40	<pre>(ix) FEATURE: (A) NAME/KEY: modified_base (B) LOCATION: 18 (D) OTHER INFORMATION: /mod_base= i</pre>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:	
45		22









(2)	INFORMATION	FOR	SEQ	ID	NO:196
-----	-------------	-----	-----	----	--------

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GGCGGATCCT TACCATTGTT TTCCTTGCCC

30

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

CGGGAATTCT GGGCTGGCCA ATGTAAA

27

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

GGCGGATCCT TATATTCCAT GGCCTGGACC

30

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA



(xi)	SEQUENCE	DESCRIPTION:	SEO	TD	NO - 199
(22-1-/	DECORPOR	DESCRIETION.	252	10	MO. LOO.

CGGGAATTCA GTATAGGAAG TCTTGGG

27

- (2) INFORMATION FOR SEQ ID NO:200:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

GGCGGATCCT TAATCACTTA GCTTTATATC

30

- (2) INFORMATION FOR SEQ ID NO:201:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

CGGGAATTCA TATCTTTGAA GCTTACC